

OM nucleic - nucleic search, using sw model
Run on: September 2, 2004, 02:56:08 ; Search time 153.864 Seconds
(without alignments)
1187.234 Million cell updates/sec

Title: US-09-801-371A-2
Perfect score: 43
Sequence: 1 tcaaaactgggctccagaa.....actgggctacagcttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3373863 seqs, 2124093041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	100.0	43	3	Aaz99817 Cis-actin
2	43	100.0	50	3	Aaz99815 Sequence
3	43	100.0	104	3	Aaz99816 Cis-actin
4	43	100.0	787	2	Aaz20979 Human TNF
5	43	100.0	815	1	Aan70075 Human ant
6	43	100.0	817	2	Aaq04340 THP-1, 3/
7	43	100.0	818	1	Aan91035 XhoI - Ps
8	43	100.0	1200	1	Aan70072 Human ant
9	43	100.0	1200	1	Aan90969 Part of g
10	43	100.0	1275	1	Aan60558 Sequence
11	43	100.0	1279	9	Ade25716 Human cDN
12	43	100.0	1323	1	Aan60363 Sequence
13	43	100.0	1324	3	Aaa34963 Human ade
14	43	100.0	1324	7	Aaf21085 Human low
15	43	100.0	1324	7	Abz96779 Human nuc
16	43	100.0	1560	1	Aan60219 Sequence
17	43	100.0	1585	1	Aan60527 Sequence
18	43	100.0	1585	1	Aan60557 Sequence
19	43	100.0	1585	7	Acac64836 Human TNF
20	43	100.0	1606	1	Aan60446 Sequence
21	43	100.0	1606	2	Aat15424 Human tum
22	43	100.0	1643	1	Aan71307 Sequence
23	43	100.0	1643	2	Aat31021 Human tum

24	43	100.0	1643	6	Abk13195 Human tum
25	43	100.0	1643	7	Acc57575 Polynucle
26	43	100.0	1643	7	Aal53712 Tumour ne
27	43	100.0	1643	7	Aad49644 Human tum
28	43	100.0	1643	9	Adc35185 Human cDN
29	43	100.0	1650	7	Acf64375 Human TNF
30	43	100.0	1666	9	Adc25664 Human cDN
31	43	100.0	2270	2	Aaz20983 ChimERIC
32	43	100.0	2570	2	Aaz20984 ChimERIC
33	43	100.0	3634	2	Aav39005 TNF-alpha
34	43	100.0	3634	2	Aax09014 Tumour ne
35	43	100.0	3634	3	AAA09014 Human tum
36	43	100.0	3634	3	AAC63770 Human TNF
37	43	100.0	3634	7	ACF63382 Human TNF
38	43	100.0	3634	7	ACC57891 Human TNF
39	43	100.0	3634	7	ACA64946 Human TNF
40	43	100.0	3634	8	ACD04988 DNA encod
41	43	100.0	6911	6	AAD45858 Human tum
42	43	100.0	6911	6	AAD45898 Human tum
43	43	100.0	7112	4	AAF86085 Lymphotox
44	43	100.0	7112	5	AAF57450 Human tum
45	43	100.0	7112	7	AAL51863 Human tum

ALIGNMENTS

RESULT 1

Aaz99817
ID Aaz99817 standard; RNA; 43 BP.

XX AC Aaz99817;

XX DT 12-JUL-2000 (first entry)

XX DE Cis-acting nucleotide sequence derived from human TNF-alpha.

XX KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
KW RNA-activated protein kinase; eukaryotic initiation factor 2; eIF2alpha;
KW tumour necrosis factor alpha; TNF-alpha; Gene therapy; ss.

XX OS Homo sapiens.

XX PN WO200014255-A1.

XX PD 16-MAR-2000.

XX PF 06-SEP-1999; 99WO-IL000483.

XX PR 07-SEP-1998; 98IL-00126112.

XX PR 26-OCT-1998; 98IL-00126757.

XX PI (YISS) YISSUM RES & DEV CO.

XX DR Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;

XX WPI; 2000-257000/22.

XX PT Regulation of gene expression by mRNA splicing is carried out using a cis
PT -acting nucleotide sequence controlled by phosphorylation of the alpha-
PT subunit of eukaryotic initiation factor 2.

XX PS Claim 5; Page 15; 75pp; English.

XX CC The specification describes a cis-acting nucleotide sequence which is
CC capable of removing introns from a precursor transcript encoded by a gene
CC which harbours at least one cis-acting nucleotide sequence. This removal
CC is effected during the production of mRNA of the gene, and depends on
CC activation of a trans-acting factor which is an RNA-activated protein
CC kinase capable of phosphorylating the alpha-subunit of eukaryotic
CC initiation factor 2 (eIF2alpha). Insertion of a cis-acting nucleotide
CC sequence, derived from the 3' untranslated region (3'UTR) of the human
CC tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders

Best Local Similarity	100.00	Pred. NO. 3.3e-07	
Matches	43	Conservative	0
Mismatches	0	Mismatches	0
Indels	0	Indels	0
Gaps	0	Gaps	0

OY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 5 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 47

RESULT 4

AAZ20979
ID AAZ20979 standard; DNA; 787 BP.
XX
AC AAZ20979;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human TNFalpha 3'UTR.
XX
KW TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
KW psoriasis; graft versus host disease; lupus erythematosus; diabetes;
KW ankylosing spondylitis; rheumatoid arthritis; ds.
XX
OS Homo sapiens.
XX
PN WO9943840-A1.
XX
PD 02-SEP-1999.
XX
PF 12-JAN-1999; 99WO-US000637.
XX
PR 27-FEB-1998; 98US-0076316P.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX
PI Tataka RJ, Marlin SD, Barton RW;
XX
DR WPI; 1999-527630/44.
XX

PT A chimeric polynucleotide consisting of a tissue necrosis factor (TNF)
promoter and an apoptosis-inducing Granzyme B polynucleotide.
XX
PS Example 1; Page 60-61; 71pp; English.
XX

CC This sequence represents a human TNFalpha (tumour necrosis factor alpha)
3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984) were
constructed comprising at least one TNFalpha promoter enhancer region
(AAZ20975-220978), a TNFalpha promoter (AAZ20972-220974), a DNA encoding
the apoptosis-inducing Granzyme B protein (AAZ20982), and a TNFalpha
3'UTR sequence. TNFalpha is one of a number of cytokines produced by
inflammatory cells. Upregulation and/or dysregulation of cytokines in
exacerbation of chronic inflammatory diseases. Introduction of the
chimeric nucleotide to activated inflammatory cells causes them to
undergo apoptosis. Pharmaceutical compositions of the chimeric nucleotide
may be useful for treating inflammatory disorders such as multiple
sclerosis, Crohn's disease, ulcerative colitis, psoriasis, graft versus
host disease, lupus erythematosus, insulin-dependent (type I) diabetes
mellitus, ankylosing spondylitis, and in particular, rheumatoid
arthritis. The use of such chimeric nucleotides offers simpler and
cheaper long-term relief, in comparison with existing conventional
pharmaceutical and invasive surgery methods

XX
SQ Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 226 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 268

RESULT 5

AAZ70075 86JP-00239154.

ID AAZ70075 standard; DNA; 815 BP.
XX
AC AAZ70075;
XX
DT 25-MAR-2003 (revised)
DT 20-JAN-1991 (first entry)
XX
DE Human anti-tumor polypeptide Xho-PstI fragment.
XX
KW Anti-tumor; cancer; cytotoxic; ss.
XX
OS Homo sapiens.
XX
PN EP247906-A.
XX
PD 02-DEC-1987.
XX
PF 04-FEB-1987; 87EP-00400261.
XX
PR 04-FEB-1986; 86JP-00021302.
PR 07-FEB-1986; 86JP-00024220.
PR 17-JUL-1986; 86JP-00169522.
XX
PA (MIZU/) MIZUNO D.
XX
PI Mizuno D, Soma GI;
XX
DR WPI; 1987-336540/48.
XX
PT Anti-tumour polypeptide(s) - prepd. using recombinant DNA prepd. from
genomic DNA of human acute leukaemia cell thp-1.
XX
PS Disclosure; Fig 7; 63pp; English.

CC The sequence is an Xho-PstI fragment of an anti-tumor protein. The
polypeptide is cytotoxic to human tumor cells but not to normal cells.
CC They are also cytotoxic to primary cell cultures obtained from metastasis
lesions of patients suffering from striated muscle tumors. They are also
resistant to all chemotherapeutic agents. See also AAZ70073-74, AAP70077-
78 and AAP95592. (Updated on 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 815 BP; 183 A; 267 C; 205 G; 160 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 1; Length 815;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 716 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 758

RESULT 6

AAQ04340
ID AAQ04340 standard; DNA; 817 BP.
XX
AC AAQ04340;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1990 (first entry)
XX
DE THP-1.

XX Acute leukaemia cell; THP-1; anti-tumour agent; ss.

XX Homo sapiens.

XX JP02088598-A.

XX 28-MAR-1990.

XX 22-SEP-1988; 86JP-00239154.

XX

PR 22-SEP-1988; 88JP-00239154.
XX PA (SOMA/) SOVA G.
XX WPI; 1990-143138/19.
XX Intrinsic TNF prodn. derivation agents - contain primer and trigger, at
PT least one of which has TNF activity.
XX PS Disclosure; Page ?; 26pp; Japanese.
XX CC Used in the prodn. of TNF prodn. agents. (Updated on 25-MAR-2003 to
CC correct PD field.)
XX SQ Sequence 817 BP; 183 A; 268 C; 206 G; 160 T; 0 U; 0 Other;
Query Match 100.0%; Score 43; DB 2; Length 817;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACCTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 716 TCAAACCTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 758
RESULT 7
AAN91035
ID AAN91035 standard; DNA; 818 BP.
XX AC AAN91035;
XX DT 27-AUG-2003 (revised)
XX DT 11-MAR-1990 (first entry)
XX DE XhoI - PstI section of gene for anti-cancer peptide.
XX KW Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
XX QS THP 1 cells.
XX XX JP01095784-A.
XX PD 13-APR-1989.
XX PF 06-OCT-1987; 87JP-00252174.
XX PR 06-OCT-1987; 87JP-00252174.
XX PA (SENG/) SEN G.
XX WPI; 1989-154899/21.
XX Novel DNA, plasmid and polypeptide(s) - useful as anticarcinogenic
PT agents.
XX PS Fig 3; Page ?; 17pp; Japanese.
XX CC Section of gene for anticarcinogenic peptide. It is genomic DNA or cDNA
CC from THP-1 cells. (Updated on 27-AUG-2003 to correct OS field.)
XX SQ Sequence 818 BP; 184 A; 268 C; 206 G; 160 T; 0 U; 0 Other;
Query Match 100.0%; Score 43; DB 1; Length 818;
Best Local Similarity 100.0%; Pred. No. 4.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACCTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 717 TCAAACCTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 759
RESULT 8
AAN70072

ID AAN70072 standard; DNA; 1200 BP.
XX AC AAN70072;
XX DT 25-MAR-2003 (revised)
XX DT 20-JAN-1991 (first entry)
XX DE Human anti-tumor polypeptide.
XX KW Anti-tumor; cancer; cytotoxic; ss.
XX OS Homo sapiens.
XX PN BP247906-A.
XX PD 02-DEC-1987.
XX PF 04-FEB-1987; 87EP-00400261.
XX PR 04-FEB-1986; 86JP-00021302.
XX PR 07-FEB-1986; 86JP-00024220.
XX PR 17-JUL-1986; 86JP-00169522.
XX PA (MIZU/) MIZUNO D.
XX PI Mizuno D, Soma GI;
XX WPI; 1987-336540/48.
XX DT Anti-tumour polypeptide(s) - prepd. using recombinant DNA prepd. from
PT genomic DNA of human acute leukaemia cell thp-1.
XX PS Disclosure; Fig 4; 63pp; English.
XX CC The polypeptide is cytotoxic to human tumor cells but not to normal
CC cells. They are also cytotoxic to primary cell cultures obtained from
CC metastasis lesions of patients suffering from striated muscle tumors.
CC They are also resistant to all chemotherapeutic agents. See also AAN70073
CC -75, AAP70077-78 and AAP95592. (Updated on 25-MAR-2003 to correct PR
CC field.)
XX SQ Sequence 1200 BP; 278 A; 329 C; 340 G; 253 T; 0 U; 0 Other;
Query Match 100.0%; Score 43; DB 1; Length 1200;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCAAACCTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 1099 TCAAACCTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 1141
RESULT 9
AAN90969
ID AAN90969 standard; DNA; 1200 BP.
XX AC AAN90969;
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 11-MAR-1990 (first entry)
XX DE Part of gene for anti-cancer peptide.
XX KW Anticarcinogenic agent; anti-cancer agent; THP-1 cells.
XX OS THP 1 cells.
XX PN JP01095784-A.
XX PD 13-APR-1989.
XX PF 06-OCT-1987; 87JP-00252174.

CC residues deleted or replaced by another AA. Plasmid pAW731 (Ser 69) is
CC claimed
XX
SQ Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 U; 0 Other;
Query Match 100.0%; Score 43; DB 1; Length 1275;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCNAACGGGGCTCGAGAACTCACTACGCTTTGA 43
| | | | |
Db 697 TCNAACGGGGCTCGAGAACTCACTACGCTTTGA 739
| | | | |

RESULT 11
AD25716
ID ADE25716 standard; cDNA; 1279 BP.
XX AC ADE25716;
XX AC
XX XX
DT 29-JAN-2004 (first entry)
XX XX
DE Human cDNA differentially expressed in foam cells #120.
XX XX
KW Human; ss; differential expression; foam cell; LPS; lipopolysaccharide;
KW cardiovascular disease; atherosclerosis.
XX OS Homo sapiens.
XX US2003194721-A1.
XX PD 16-OCT-2003.
XX PF 18-SEP-2002; 2002US-00247671.
XX PR 19-SEP-2001; 2001US-0323784P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Mikita T, Shiffman D, Porter JG, Kaser MR;
XX WPI; 2003-875398/81.
DR P-PSDB; ADE25778.
DR
XX
PT Combination containing several polynucleotide that are differentially
PT expressed in foam cells and complements of the polynucleotides, useful
PT for diagnosing cardiovascular disease or atherosclerosis.
PS Claim 1; SEQ ID NO 120; 37pp; English.
PS
XX The invention relates to a combination comprising several polynucleotides
CC having any one of 127 sequences (SI) such as the sequence of human
CC calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4
CC hydrolase, human CGR-142 protein mRNA, human K+ channel beat 2 subunit
CC mRNA, etc., and their complements. The cDNAs are differentially expressed
CC in LPS (lipopolysaccharide)-treated foam cells. Also included are
CC obtaining an extended or full length gene from a library of nucleic acid
CC sequences, an expression vector containing the nucleic acids, a host cell
CC containing the vector, a purified polypeptide appearing as ADE25750 and
CC ADE25751, producing a protein by culturing the host cell, and a
CC composition comprising a purified antibody that specifically binds to the
CC proteins. The foam cell-expressed nucleic acids are useful for a high
CC throughput detection of differential expression of one or more
CC polynucleotides in a sample. The sample is from a subject with
CC atherosclerosis and comparison with a standard defines early, mid or late
CC stages of the disorder. The foam cell-expressed nucleic acids are useful
CC for high throughput screening of a library of molecules or compounds to
CC identify a ligand which binds a polynucleotide. The library is chosen
CC from DNA molecules, peptides, proteins and RNA molecules. The protein is
CC useful for a high throughput screening of library of molecules or
CC compounds to identify at least one ligand which specifically binds a
CC foam cell, for purifying a ligand from a sample for making an antibody. The
CC foam cell-expressed nucleic acids are useful for diagnosing

CC cardiovascular disorder. The foam cell-expressed nucleic acids are useful
 CC as elements on a microarray which can be used for detecting related
 CC polynucleotide in a sample, diagnosing cardiovascular disease,
 CC atherosclerosis. The present sequence represents a cDNA whose expression
 CC is upregulated in LPS treated foam cells.

XX Sequence 1279 BP; 293 A; 415 C; 323 G; 248 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 9; Length 1279;
 Best Local Similarity 100.0%; Pred. No. 5.2e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCARACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
 Db 1081 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 1123

RESULT 12

AAAN60363
 ID AAN60363 standard; DNA; 1323 BP.

XX AC AAN60363;

XX DT 19-JUN-1991 (first entry)

XX Sequence encoding human tumour necrosis factor.

XX hTNF; tumour; cancer; interferon; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..534

FT sig_peptide 1..80

FT mat_peptide 61..534

FT label= Secretory leader peptide

FT tag= c

XX EP168214-A.

XX 15-JAN-1986.

XX 03-JUL-1985; 85EP-00304758.

XX 05-JUL-1984; 84US-00627959.

XX 05-JUL-1984; 84US-00628059.

XX 05-JUL-1984; 84US-00628060.

XX 03-DEC-1984; 84US-00677156.

XX 03-DEC-1984; 84US-00677257.

XX 03-DEC-1984; 84US-00677267.

XX 03-DEC-1984; 84US-00677454.

XX (GETH) GENENTECH INC.

XX Aggarwal BB, Lee SH, Goeddel DV, Nedwin GE;

XX WPI; 1986-015483/03.

XX P-PSDB; AAP60417.

XX Pure tumour necrosis factor and mutant forms - new DNA coding sequences

XX and transformed cells.

XX Claim 20; Fig 10; 90pp; English.

XX Sequence encodes the pure human tumour necrosis factor, mutants of which

XX are covered by the claims. TNF and mutants are useful in treating

XX tumours, especially in tandem with interferon. The encoding sequence may

XX be used to create plasmid pTRPXA-TNF, allowing transformation of an

XX E.coli host for the expression of TNF

XX Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 1; Length 1323;
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCARACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
 Db 754 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 796

RESULT 13

AAA34963
 ID AAA34963 standard; DNA; 1324 BP.

XX AC AAA34963;

XX DT 28-JUL-2000 (first entry)

XX Human adenosine receptor related polynucleotide SEQ ID NO:2652.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 XX phosphorothioate; impaired respiration; inflammation; allergy;
 XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 XX antiallergic; antiasthmatic; cytosolic; analgesic; impaired airway;
 XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

XX WO200009525-A2.

XX 24-FEB-2000.

XX 03-AUG-1999; 99WO-US017712.

XX 03-AUG-1998; 98US-0095212P.

XX (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary

XX vasoconstriction, inflammation, allergies, asthma, hypertension, or

XX bronchitis, emphysema, respiratory distress syndrome, ischemia or

XX cancers.

XX Disclosure; Page 814-815; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
 XX oligonucleotide (ON) with low adenosine (up to 15%), which targets
 XX nucleic acids involved in bronchoconstriction, allergies, and/or
 XX inflammation. The ON can have antiinflammatory, antiallergic,
 XX antiasthmatic, cytosolic and analgesic activities. The compositions are
 XX useful for the treatment of diseases associated with inflammation,
 XX impaired airways, including lung disease and diseases whose secondary
 XX effects afflict the lungs of a subject. They can be used for treating
 XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 XX impaired respiration, respiratory distress syndrome, pain, cystic
 XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 XX pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 XX carcinomas, and cancers which may metastasize to the lungs, including
 XX breast and prostate cancer. The reduction of the adenosine content of the
 XX ONs reduces side effects. The A-containing ONs break down with the
 XX release of deoxyadenosine which activates adenosine receptors causing
 XX bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 XX nucleotide sequences given in the sequence listing from the present
 XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 XX sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 XX from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to

CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
 Query Match 100.0%; Score 43; DB 3; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
 DB 755 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 797
 RESULT 14
 AAF21085
 ID AAF21085 standard; DNA; 1324 BP.
 XX AAF21085;
 XX
 DT 14-MAR-2001 (first entry)
 XX Human low adenosine antisense oligonucleotide related sequence #2652.
 DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 XX human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytosatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 PN WO200062736-A2.
 XX
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US008020.
 PF
 XX 06-APR-1999; 99US-0127958P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 XX Disclosure; Page 887; 1592pp; English.
 PS
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytosatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central

CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
 Query Match 100.0%; Score 43; DB 3; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
 DB 755 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 797
 RESULT 15
 ABZ96779
 ID ABZ96779 standard; DNA; 1324 BP.
 XX ABZ96779;
 AC
 XX 17-OCT-2003 (first entry)
 DT
 XX Human nucleic acid sequence.
 DE
 XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytosatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 XX Homo sapiens.
 OS
 XX WO200285308-A2.
 PN
 XX 31-OCT-2002.
 PD
 XX 23-APR-2002; 2002WO-US013135.
 PF
 XX 24-APR-2001; 2001US-0286137P.
 PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 PI
 XX WPI; 2003-229219/22.
 DR
 XX Pharmaceutical composition for treating ailments associated with impaired
 CC respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX Disclosure; SEQ ID NO 12021; 872pp; English.
 PS
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 43; DB 7; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 5.3e-07;
 Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTCAGCTTTGA 43
 DB 755 TCAAACTGGGGCTCCAGAACTCACTGGGGCTCAGCTTTGA 797

Search completed: September 2, 2004, 08:05:12
 Job time : 154.864 secs

OM nucleic - nucleic search, using sw model

Run on: September 13, 2004, 12:13:03 ; Search time 159.422 Seconds
(without alignments)
1357.126 Million cell updates/sec

Title: US-09-801-371A-2
Perfect score: 43
Sequence: 1 tcaaaactggggcctccagaa.....actggggcctacagctttga 43

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues

Total number of hits satisfying chosen parameters: 6608766

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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5:	/cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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11:	/cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
13:	/cgn2_6/prodata/2/pubpna/US09_PUBCOMB.seq:*
14:	/cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq:*
15:	/cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq:*
16:	/cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
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19:	/cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	43	100.0	43	9	US-09-801-371A-2
2	43	100.0	43	9	US-09-801-371A-6
3	43	100.0	50	9	US-09-801-371A-8
4	43	100.0	81	9	US-09-801-371A-7
5	43	100.0	104	9	US-09-801-371A-1
6	43	100.0	104	9	US-09-801-371A-5
7	43	100.0	787	13	US-10-356-308A-13
8	43	100.0	1279	15	US-10-247-671-120
9	43	100.0	1585	13	US-10-342-887-501
10	43	100.0	1585	13	US-10-172-118-501
11	43	100.0	1585	17	US-10-641-643-1329
12	43	100.0	1643	13	US-10-242-887-1901
13	43	100.0	1643	13	US-10-172-118-1901
14	43	100.0	1643	15	US-10-272-411-4

15	43	100.0	1643	15	US-10-218-547-3	Sequence 3, Appli
16	43	100.0	1643	15	US-10-272-328A-4	Sequence 4, Appli
17	43	100.0	1643	15	US-10-310-793-9	Sequence 9, Appli
18	43	100.0	1666	15	US-10-247-671-68	Sequence 68, Appli
19	43	100.0	2088	13	US-09-973-850-1	Sequence 1, Appli
20	43	100.0	2088	13	US-09-973-850-2	Sequence 2, Appli
21	43	100.0	2088	13	US-09-973-850-3	Sequence 3, Appli
22	43	100.0	3634	10	US-09-824-322B-1	Sequence 1, Appli
23	43	100.0	3634	10	US-09-932-300-34	Sequence 34, Appli
24	43	100.0	3634	13	US-10-202-062-3	Sequence 3, Appli
25	43	100.0	3634	16	US-10-191-997-104	Sequence 104, Appli
26	43	100.0	3634	17	US-10-652-795-1	Sequence 1, Appli
27	43	100.0	3634	17	US-10-647-918-1	Sequence 1, Appli
28	43	100.0	4830	16	US-10-429-802-33	Sequence 33, Appli
29	43	100.0	4830	16	US-10-430-503-24	Sequence 24, Appli
30	43	100.0	22173	17	US-10-322-696-228	Sequence 28, Appli
31	35	81.4	418	9	US-09-796-692-6223	Sequence 6223, Ap
32	35	81.4	418	15	US-10-040-862-6223	Sequence 6223, Ap
33	35	81.4	418	16	US-10-057-475B-6223	Sequence 6223, Ap
34	35	81.4	418	16	US-10-154-884B-6223	Sequence 6223, Ap
35	30.6	71.2	51	9	US-09-801-371A-10	Sequence 10, Appli
36	25.4	59.1	3673778	15	US-10-312-841-2	Sequence 2, Appli
37	23	53.5	260	10	US-09-535-459-1127	Sequence 1127, Ap
38	22.8	53.0	696	13	US-10-027-632-110108	Sequence 110108,
39	22.8	53.0	696	16	US-10-027-632-110108	Sequence 110108,
40	22.6	52.6	232	13	US-10-085-783A-46829	Sequence 46829, A
41	22.6	52.6	232	16	US-10-242-535A-46829	Sequence 46829, A
42	22.6	52.6	612	13	US-10-027-632-110698	Sequence 110698,
43	22.6	52.6	612	16	US-10-027-632-110698	Sequence 110698,
44	22.4	52.1	922	13	US-10-027-632-120081	Sequence 120081,
45	22.4	52.1	922	16	US-10-027-632-120081	Sequence 120081,

ALIGNMENTS

RESULT 1
US-09-801-371A-2
; Sequence 2, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Naysf
; APPLICANT: Ben-Assouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801.371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-2

Query Match 100.0%; Score 43; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 43
DB 1 TCAAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGA 43

RESULT 2
US-09-801-371A-6/c
; Sequence 6, Application US/09801371A
; Patent No. US20020155569A1

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; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-6

Query Match 100.0%; Score 43; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 43 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1

RESULT 3
US-09-801-371A-8
; Sequence 8, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: RNA
; ORGANISM: Homo sapien
US-09-801-371A-8

Query Match 100.0%; Score 43; DB 9; Length 50;
Best Local Similarity 79.1%; Pred. No. 8.3e-08;
Matches 34; Conservative 9; Mismatches 0; Indels 0; Caps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 5 UCAAAACUGGGCCCUCCAGAACUCACUGGGGCCCUACAGCUUGA 47

RESULT 4
US-09-801-371A-7
; Sequence 7, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; TITLE OF INVENTION: MANIPULATION OF MRNA SPLICING AND ITS USES

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; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-5

Query Match 100.0%; Score 43; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 100 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 58

RESULT 7
US-10-356-308A-13
; Sequence 13, Application US/10356308A
; Publication No. US20040039186A1
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall Wilber
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/121-1-CIP1
; CURRENT APPLICATION NUMBER: US/10/356,308A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/032,297
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: US 60/039,266
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 13
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Homo sapiens
; LOCATION: 1 to 787
; OTHER INFORMATION: TNFa 3' untranslated region
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E., et al.
; JOURNAL: Nucleic Acid Research
; VOLUME: 13
; PAGES: 6361-6373
; DATE: 1985
US-10-356-308A-13

Query Match 100.0%; Score 43; DB 13; Length 787;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268

RESULT 8
US-10-247-671-120
; Sequence 120, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186

; SOFTWARE: PERL Program
; SEQ ID NO 120
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inocyte ID No. US20030194721A1 561301CB1
US-10-247-671-120

Query Match 100.0%; Score 43; DB 15; Length 1279;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 1081 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1123

RESULT 9
US-10-342-887-501
; Sequence 501, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-501

Query Match 100.0%; Score 43; DB 13; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049

RESULT 10
US-10-172-118-501
; Sequence 501, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999

;; CURRENT APPLICATION NUMBER: US/10/172,118
;; CURRENT FILING DATE: 2002-06-14
;; PRIOR APPLICATION NUMBER: 60/380,770
;; PRIOR FILING DATE: 2002-05-14
;; NUMBER OF SEQ ID NOS: 2699
;; SEQ ID NO 501
;; LENGTH: 1585
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: NM_000594
;; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-501

Query Match 100.0%; Score 43; DB 13; Length 1585;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 1007 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 1049

RESULT 11
US-10-641-643-1329
;; Sequence 1329, Application US/10641543
;; Publication No. US20040077003A1
;; GENERAL INFORMATION:
;; APPLICANT: Cocks, Benjamin G.
;; Susan G. Stuart
;; Jeffrey J. Seilhaner
;; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
;; NUMBER OF SEQUENCES: 1508
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;; STREET: 3174 PORTER DRIVE
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: USA
;; ZIP: 94304

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/641,643
;; FILING DATE: 14-Aug-2003
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: <Unknown>
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Zeller, Karen J.
;; REGISTRATION NUMBER: 37,071
;; REFERENCE/DOCKET NUMBER: PA-0001 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (650) 855-0555
;; TELEFAX: (650) 845-4166
;; INFORMATION FOR SEQ ID NO: 1329:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1585 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: GENBANK
;; CLONE: 9329737

;; SEQUENCE DESCRIPTION: SEQ ID NO: 1329 :
US-10-641-643-1329

Query Match 100.0%; Score 43; DB 17; Length 1585;

Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 1007 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 1049

RESULT 12
US-10-342-887-1901
;; Sequence 1901, Application US/10342887
;; Publication No. US20040058340A1
;; GENERAL INFORMATION:
;; APPLICANT: Dai, Hongyue
;; APPLICANT: He, Yudong
;; APPLICANT: Linsley, Peter S.
;; APPLICANT: Mao, Mao
;; APPLICANT: Roberts, Christopher J.
;; APPLICANT: Van 't Veer, Laura Johanna
;; APPLICANT: Van de Vijver, Marc J.
;; APPLICANT: Bernards, Rene
;; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;; FILE REFERENCE: 9301-188-999
;; CURRENT APPLICATION NUMBER: US/10/342,887
;; CURRENT FILING DATE: 2003-01-15
;; PRIOR APPLICATION NUMBER: 60/298,918
;; PRIOR FILING DATE: 2001-06-18
;; PRIOR APPLICATION NUMBER: 60/380,710
;; PRIOR FILING DATE: 2002-05-14
;; PRIOR APPLICATION NUMBER: 10/172,118
;; PRIOR FILING DATE: 2002-06-14
;; NUMBER OF SEQ ID NOS: 2699
;; SEQ ID NO 1901
;; LENGTH: 1643
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-342-887-1901

Query Match 100.0%; Score 43; DB 13; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
DB 1074 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 1116

RESULT 13
US-10-172-118-1901
;; Sequence 1901, Application US/10172118
;; Publication No. US20030224374A1
;; GENERAL INFORMATION:
;; APPLICANT: Dai, Hongyue
;; APPLICANT: He, Yudong
;; APPLICANT: Linsley, Peter
;; APPLICANT: Mao, Mao
;; APPLICANT: Roberts, Chris
;; APPLICANT: Van 't Veer, Laura
;; APPLICANT: Van de Vijver, Marc
;; APPLICANT: Bernards, Rene
;; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;; FILE REFERENCE: 9301-175-999
;; CURRENT APPLICATION NUMBER: US/10/172,118
;; CURRENT FILING DATE: 2002-06-14
;; PRIOR APPLICATION NUMBER: 60/380,770
;; PRIOR FILING DATE: 2002-05-14
;; NUMBER OF SEQ ID NOS: 2699
;; SEQ ID NO 1901
;; LENGTH: 1643
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; PUBLICATION INFORMATION:
;; DATABASE ACCESSION NUMBER: X01394

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; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1901

Query Match      100.0%; Score 43; DB 13; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db      1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 14
US-10-272-411-4
; Sequence 4, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIXICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272,411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ X01394.1
; DATABASE ENTRY DATE: 1995-03-21
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
; DATABASE ENTRY DATE: 2002-05-01
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ M35592.1
; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
; DATABASE ENTRY DATE: 2002-08-01
; RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4

Query Match      100.0%; Score 43; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db      1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 15
US-10-218-547-3
; Sequence 3, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
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; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
US-10-218-547-3

Query Match      100.0%; Score 43; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db      1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

Search completed: September 13, 2004, 16:11:26
Job time : 161.422 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2004, 02:02:56 ; Search time 25.449 Seconds
(without alignments)
937.676 Million cell updates/sec

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Title: US-09-801-371A-2
Perfect score: 43
Sequence: 1 tcaactggggcctccagaa.....actgggcctacagattga 43

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

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Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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2: /csm2_6/ptodata/2/ina/5B_COMB.seq.*
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5: /csm2_6/ptodata/2/ina/PCRTUS_COMB.seq.*
6: /csm2_6/ptodata/2/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	43	100.0	787	4	US-09-032-297A-13	Sequence 13, Appl
2	43	100.0	787	4	US-09-229-151C-7	Sequence 7, Appl
3	43	100.0	1585	4	US-09-023-65S-1329	Sequence 1329, Ap
4	43	100.0	1643	3	US-08-880-342-36	Sequence 36, Appl
5	43	100.0	1643	4	US-09-505-250-4	Sequence 4, Appl
6	43	100.0	2270	4	US-09-229-151C-13	Sequence 13, Appl
7	43	100.0	2570	4	US-09-229-151C-14	Sequence 14, Appl
8	43	100.0	3634	3	US-09-166-186-1	Sequence 1, Appl
9	43	100.0	3634	3	US-09-313-932-1	Sequence 1, Appl
10	43	100.0	3634	3	US-09-109-663-34	Sequence 34, Appl
C 11	21.4	49.8	1274	4	US-09-148-545-72	Sequence 72, Appl
C 12	21.4	49.8	1296	4	US-09-148-545-126	Sequence 126, App
13	21.4	49.8	24707	4	US-09-740-027-3	Sequence 3, Appl
14	21	48.8	771	5	PCT-US95-12987-1	Sequence 1, Appl
15	21	48.8	771	5	PCT-US95-12987-3	Sequence 3, Appl
16	21	48.8	771	5	PCT-US95-12987-5	Sequence 5, Appl
17	20.8	48.4	493	4	US-09-621-976-978	Sequence 978, App
18	20.8	48.4	509	4	US-09-621-976-2765	Sequence 2765, Ap
19	20.8	48.4	534	4	US-09-621-976-714	Sequence 714, App
20	20.8	48.4	557	4	US-09-833-381-551	Sequence 551, App
C 21	20.8	48.4	861	1	US-08-409-731A-1	Sequence 1, Appl
22	20.8	48.4	861	2	US-08-470-298B-1	Sequence 1, Appl
23	20.8	48.4	861	3	US-09-023-073A-1	Sequence 1, Appl
24	20.8	48.4	861	3	US-09-361-737-1	Sequence 1, Appl
25	20.8	48.4	944	2	US-08-920-825-1	Sequence 1, Appl
26	20.8	48.4	944	3	US-09-807-817-1	Sequence 1, Appl
27	20.8	48.4	944	4	US-09-734-036-1	Sequence 1, Appl

28	20.8	48.4	957	3	US-08-899-031-2	Sequence 2, Appl1
29	20.8	48.4	1327	4	US-08-783-161-3	Sequence 1346, App
C 29	20.8	48.4	65042	4	US-08-784-186-3	Sequence 3, Appl1
C 31	20	46.5	20	3	US-08-166-186-32	Sequence 32, Appl1
C 32	20	46.5	20	3	US-08-166-186-212	Sequence 212, App
C 33	20	46.5	20	3	US-08-166-186-213	Sequence 213, App
C 34	20	46.5	20	3	US-08-166-186-214	Sequence 214, App
C 35	20	46.5	20	3	US-09-313-932-32	Sequence 32, Appl1
C 36	20	46.5	20	3	US-09-313-932-212	Sequence 212, App
C 37	20	46.5	20	3	US-09-313-932-213	Sequence 213, App
C 38	20	46.5	20	3	US-09-313-932-214	Sequence 214, App
C 39	20	46.5	20	3	US-09-313-932-354	Sequence 354, App
C 40	20	46.5	20	3	US-09-313-932-357	Sequence 357, App
C 41	20	46.5	20	3	US-09-313-932-358	Sequence 358, App
C 42	20	46.5	20	3	US-09-313-932-361	Sequence 361, App
C 43	20	46.5	20	3	US-09-313-932-468	Sequence 468, App
C 44	19.8	46.0	459	4	US-09-621-976-979	Sequence 979, App
C 45	19.8	46.0	3271	4	US-09-548-977B-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-09-032-297A-13
; Sequence 13, Application US/09032297A
; Patent No. 6525184
; GENERAL INFORMATION:
; APPLICANT: Revati J. Tatake, Steven D. Marlin and
; Randall W. Barton
; TITLE OF INVENTION: Self-Regulated Apoptosis of
; Inflammatory Cells by Gene Therapy
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Boehringer Ingelheim Corporation
; STREET: 900 Ridgebury Road, P.O. Box 368
; CITY: Ridgefield
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06877-0368
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032.297A
; FILING DATE: 27-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,265
; FILING DATE: 28-FEB-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert P. Raymond
; REGISTRATION NUMBER: 25089
; REFERENCE/DOCKET NUMBER: 9/12/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-731-6183
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: <Unknown>
; DESCRIPTION: DNA
; FEATURE:
; NAME/KEY: TNFA 3' untranslated region
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-032-297A-13

Query Match 100.0%; Score 43; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.7e+08;

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Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268
|||||

RESULT 2
US-09-229-151C-7
; Sequence 7, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Barton, Steven D.
; APPLICANT: Marlin, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 7
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: TNF-alpha untranslated region
US-09-229-151C-7

Query Match 100.0%; Score 43; DB 4; Length 787;
Best Local Similarity 100.0%; Pred. No. 1.7e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
|||||
Db 226 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 268
|||||

RESULT 3
US-09-023-655-1329
; Sequence 1329, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1329:
SEQUENCE CHARACTERISTICS:
LENGTH: 1585 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9339737
US-09-023-655-1329

Query Match 100.0%; Score 43; DB 4; Length 1585;
Best Local Similarity 100.0%; Pred. No. 1.9e-08; Mismatches 0; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
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Db 1007 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1049
|||||

RESULT 4
US-08-880-342-36
; Sequence 36, Application US/08880342
; Patent No. 6218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 8255-0018.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown

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; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE: TNF CDNA HSTNFR (EMBL Accession
; INDIVIDUAL ISOLATE: #X01394)
; INDIVIDUAL ISOLATE: #X01394)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 153..851
; US-08-880-342-36

Query Match      100.0%; Score 43; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.9e-08; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 5
US-09-505-250-4
; Sequence 4, Application US/09505250A
; Patent No. 6329148
; GENERAL INFORMATION:
; APPLICANT: Rosen, Glenn
; APPLICANT: Kao, Peter
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
; TITLE OF INVENTION: Triptolides and Death Domain Ligands
; FILE REFERENCE: SUN-109PRV2
; CURRENT APPLICATION NUMBER: US/09/505,250A
; CURRENT FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (153)...(854)
US-09-505-250-4

Query Match      100.0%; Score 43; DB 4; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.9e-08; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 1074 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1116

RESULT 6
US-09-229-151C-13
; Sequence 13, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 13
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Human
; FEATURE:

; OTHER INFORMATION: chimeric gene : -706TNFpGB3'UTR
US-09-229-151C-13

Query Match      100.0%; Score 43; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 2.1e-08; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 1709 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 1751

RESULT 7
US-09-229-151C-14
; Sequence 14, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 14
; LENGTH: 2570
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: chimeric gene : -1005TNFpGB3'UTR
US-09-229-151C-14

Query Match      100.0%; Score 43; DB 4; Length 2570;
Best Local Similarity 100.0%; Pred. No. 2.1e-08; Indels 0; Gaps 0;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 43
Db 2009 TCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGA 2051

RESULT 8
US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
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/ NAME/KEY: exon
/ LOCATION: (1589)..(1634)
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (1635)..(1821)
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (1822)..(1869)
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (1870)..(2070)
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (2171)..(3381)
/ PUBLICATION INFORMATION:
/ AUTHORS: Nedwin, G.E.
/ AUTHORS: Naylor, S.L.
/ AUTHORS: Sakaguchi, A.Y.
/ AUTHORS: Smith, D.
/ AUTHORS: Jarrett-Nedwin, J.
/ AUTHORS: Pennica, D.
/ AUTHORS: Goeddel, D.V.
/ AUTHORS: Gray, P.W.
/ TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
/ TITLE: structure and chromosomal localization
/ JOURNAL: Nucleic Acids Res.
/ VOLUME: 13
/ ISSUE: 17
/ PAGES: 6361-6373
/ DATE: 1985-09-11
/ DATABASE ACCESSION NUMBER: X02910 Genbank
/ DATABASE ENTRY DATE: 1997-02-17
US-09-166-186-1
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Query Match 100.0%; Score 43; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
Db 2812 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 2854
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RESULT 9
US-09-313-932-1
/ Sequence 1, Application US/09313932A
/ Patent No. 6228642
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Brenda
/ APPLICANT: Bennett, C. Frank
/ APPLICANT: Butler, Madeline M.
/ APPLICANT: Shanahan, William R.
/ TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TNF-
/ FILE REFERENCE: ISPH-0356
/ CURRENT APPLICATION NUMBER: US/09/313,932A
/ CURRENT FILING DATE: 1999-05-18
/ NUMBER OF SEQ ID NOS: 501
/ SEQ ID NO 1
/ LENGTH: 3634
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (796...981,1589...1634,1822...1869,2171...2592)
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (615)..(981)
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (982)..(1588)
/ FEATURE:
/ NAME/KEY: exon
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/ LOCATION: (1589)..(1634)
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (1635)..(1821)
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (1822)..(1869)
/ FEATURE:
/ NAME/KEY: intron
/ LOCATION: (1870)..(2070)
/ FEATURE:
/ NAME/KEY: exon
/ LOCATION: (2171)..(3381)
/ PUBLICATION INFORMATION:
/ AUTHORS: Nedwin, G.E.
/ AUTHORS: Naylor, S.L.
/ AUTHORS: Sakaguchi, A.Y.
/ AUTHORS: Smith, D.
/ AUTHORS: Jarrett-Nedwin, J.
/ AUTHORS: Pennica, D.
/ AUTHORS: Goeddel, D.V.
/ AUTHORS: Gray, P.W.
/ TITLE: Human lymphotoxin and tumor necrosis factor genes:
/ TITLE: structure, homology and chromosomal localization
/ JOURNAL: Nucleic Acids Res.
/ VOLUME: 13
/ ISSUE: 17
/ PAGES: 6361-6373
/ DATE: 1985-09-11
/ DATABASE ACCESSION NUMBER: X02910 Genbank
/ DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1
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Best Local Similarity 100.0%; Pred. No. 2.2e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 43
Db 2812 TCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGA 2854
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RESULT 10
US-09-109-663-34
/ Sequence 34, Application US/09109663
/ Patent No. 6277981
/ GENERAL INFORMATION:
/ APPLICANT: Tu, Guang-Chou
/ APPLICANT: Israel, Yedy
/ TITLE OF INVENTION: AN IMPROVED METHOD FOR DESIGN AND SELECTION OF
/ TITLE OF INVENTION: EFFICACIOUS ANTISENSE OLIGONUCLEOTIDES
/ FILE REFERENCE: 9855-3U1
/ CURRENT APPLICATION NUMBER: US/09/109,663
/ CURRENT FILING DATE: 1998-07-03
/ EARLIER APPLICATION NUMBER: 60/051,705
/ EARLIER FILING DATE: 1997-07-03
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 34
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/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: TNF(alpha) cDNA
US-09-109-663-34
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Best Local Similarity 100.0%; Pred. No. 2.2e-08;
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; Patent No. 6590075
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2001P1
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; EARLIER FILING DATE: 1998-03-06
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70	EARLIER FILING DATE: 1997-05-23
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72	EARLIER FILING DATE: 05-Sep-1997
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74	EARLIER FILING DATE: 1997-05-23
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46 EARLIER APPLICATION NUMBER: 60/056,884
47 EARLIER FILING DATE: 1997-08-22
48 NUMBER OF SEQ ID NOS: 280
49 SOFTWARE: PatentIn Ver. 2.0
50 SEQ ID NO 126
51 LENGTH: 1296

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; Patent No. 6485939
; GENERAL INFORMATION
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN
; TITLE OF INVENTION: PROTEINS, NUC
; TITLE OF INVENTION: COPOLYMER PRO
; FILE REFERENCE: CL001052
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2000-12-20

; NUMBER OF SEQ ID NOS: 4
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; SEQ ID NO 3
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; TYPE: DNA
; ORGANISM: Human
US-09-740-027-3

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; Sequence 1, Application PC/TUS9512987
; GENERAL INFORMATION:
; APPLICANT: LAFEMINA, R.
; APPLICANT: SARDANA, V.
; APPLICANT: VELOSKI, C.
; TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12987
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEREDITH, ROY D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 19262 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; HYPOTHEtical: NO
; ANTI-SENSE: NO
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; Sequence 3, Application PC/TUS9512987
; GENERAL INFORMATION:
; APPLICANT: LAFEMINA, R.

; APPLICANT: SARDANA, V.
; APPLICANT: VELOSKI, C.
; TITLE OF INVENTION: STABLE RECOMBINANT HCMV PROTEASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROY D. MEREDITH
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVE.
; CITY: RAHWAY
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07065-0907
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; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12987
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MEREDITH, ROY D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: 19262 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-4678
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; HYPOTHEtical: NO
; ANTI-SENSE: NO
PCT-US95-12987-3

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Best Local Similarity 73.0%; Pred. No. 16;
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Job time : 26.449 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	104	100.0	1585	17	US-10-641-643-1329
7	104	100.0	1643	13	US-10-342-687-1301
8	104	100.0	1643	13	US-10-172-118-1901
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10	104	100.0	1643	15	US-10-218-547-3
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21	104	100.0	3634	17	US-10-652-795-1	Sequence 1, Appli	
22	104	100.0	3634	17	US-10-647-918-1	Sequence 1, Appli	
23	104	100.0	4830	16	US-10-429-802-33	Sequence 33, Appli	
24	104	100.0	4830	16	US-10-430-503-24	Sequence 24, Appli	
25	104	100.0	22173	17	US-10-322-696-28	Sequence 28, Appli	
c	26	93	89.4	1279	15	US-10-247-671-120	Sequence 120, App
	27	77	74.0	81	9	US-09-801-371A-7	Sequence 7, Appli
28	59.8	57.5	3673778	15	US-10-312-841-1	Sequence 1, Appli	
c	29	58.2	3673778	15	US-10-312-841-2	Sequence 2, Appli	
30	50	48.1	50	9	US-09-801-371A-8	Sequence 8, Appli	
31	43	41.3	43	9	US-09-801-371A-2	Sequence 2, Appli	
c	32	43	41.3	43	9	US-09-801-371A-6	Sequence 6, Appli
33	42	40.4	418	9	US-09-796-692-6223	Sequence 6223, Ap	
34	42	40.4	418	15	US-10-040-862-6223	Sequence 6223, Ap	
35	42	40.4	418	16	US-10-057-475B-6223	Sequence 6223, Ap	
36	42	40.4	418	16	US-10-154-884B-6223	Sequence 6223, Ap	
37	33	31.7	51	9	US-09-801-371A-10	Sequence 10, Appl	
c	38	31.2	30.0	90043	13	US-10-087-192-1141	Sequence 1141, Ap
c	39	31	29.8	418550	16	US-10-292-798-1463	Sequence 1463, Ap
40	30.4	29.2	440	16	US-10-062-674-37	Sequence 37, Appli	
41	30.2	29.0	45855	16	US-10-085-117-316	Sequence 316, App	
c	42	29.6	28.5	2127	13	US-10-282-122A-33764	Sequence 33764, A
c	43	29.2	28.1	525	13	US-10-424-599-60620	Sequence 60620, A
c	44	29.2	28.1	923	13	US-10-424-599-2207	Sequence 2207, Ap
c	45	29.2	28.1	1287	13	US-10-424-599-2206	Sequence 2206, Ap

ALIGNMENTS

RESULT 1
US-09-801-371A-1
; Sequence 1, Application US/09801371A
; Patent No. US20020155569A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801.371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-371A-1

Query Match	100.0%	Score 104;	DB 9;	Length 104;
Best Local Similarity	100.0%	Pred. No. 7.2e-28;		
Matches 104;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GAATTCAACTGGGGCCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG	60	
Db	1	GAATTCAACTGGGGCCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG	60	
QY	61	GAATTCGAGACCGAGGAGCCTTTGGTCTCGCCAGATGCTGC	104	
Db	61	GAATTCGAGACCGAGGAGCCTTTGGTCTCGCCAGATGCTGC	104	

RESULT 2

US-09-801-371A-5/c
; Sequence 5, Application US/09801371A
; Patent No. US2002015569A1
; GENERAL INFORMATION:
; APPLICANT: Kaemfer, Raymond
; APPLICANT: Osman, Farhat
; APPLICANT: Jarrous, Nayef
; APPLICANT: Ben-Asouli, Yitzhak
; TITLE OF INVENTION: REGULATION OF GENE EXPRESSION THROUGH
; FILE REFERENCE: A34084-PCT-USA-A 066031.0147
; CURRENT APPLICATION NUMBER: US/09/801,371A
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT WO 00/14255
; PRIOR FILING DATE: 1999-09-06
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 104
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-801-371A-5

Query Match 100.0%; Score 104; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 7.2e-28;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 104 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 45
QY 61 GAATCTGGAGACCCAGGAGCCCTTTGGTCTGCCAGAAATGCTGC 104
DB 44 GAATCTGGAGACCCAGGAGCCCTTTGGTCTGCCAGAAATGCTGC 1

RESULT 3

US-10-356-308A-13
; Sequence 13, Application US/10356308A
; Publication No. US20040039186A1
; GENERAL INFORMATION:
; APPLICANT: Tataka, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall Wilber
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/121-1-CIP1
; CURRENT APPLICATION NUMBER: US/10/356,308A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 09/032,297
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: US 60/039,266
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Homo sapiens
; LOCATION: 1 to 787
; OTHER INFORMATION: TNPa 3' untranslated region
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E., et al.
; JOURNAL: Nucleic Acid Research
; VOLUME: 13
; PAGES: 6361-6373
; DATE: 1985
US-10-356-308A-13

Query Match 100.0%; Score 104; DB 13; Length 787;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
222 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 281
QY 61 GAATCTGGAGACCCAGGAGCCCTTTGGTCTGCCAGAAATGCTGC 104
DB 282 GAATCTGGAGACCCAGGAGCCCTTTGGTCTGCCAGAAATGCTGC 325

RESULT 4

US-10-342-887-501
; Sequence 501, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-501

Query Match 100.0%; Score 104; DB 13; Length 1585;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1062
QY 61 GAATCTGGAGACCCAGGAGCCCTTTGGTCTGCCAGAAATGCTGC 104
DB 1063 GAATCTGGAGACCCAGGAGCCCTTTGGTCTGCCAGAAATGCTGC 1106

RESULT 5

US-10-172-118-501
; Sequence 501, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699

Query Match 100.0%; Score 104; DB 13; Length 1585;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; SEQ ID NO 501
; LENGTH: 1585
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_000594
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-501

Query Match      100.0%; Score 104; DB 13; Length 1585;
Best Local Similarity 100.0%; Pred. NO. 1.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACCTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCTGACATCTG 60
Db 1003 GAATTCAAACCTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTGATCCCTGACATCTG 1062

QY 61 GAATCTGGAGACACGGAGAGCTTTGGTTCTGGCCAGAAATCTGC 104
Db 1063 GAATCTGGAGACACGGAGAGCTTTGGTTCTGGCCAGAAATCTGC 1106

RESULT 6
US-10-641-643-1329
; Sequence 1329, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Sellhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641.643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1329:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: GENBANK
; LIBRARY: 9339737
; SEQUENCE DESCRIPTION: SEQ ID NO: 1329 :
US-10-641-643-1329

Query Match      100.0%; Score 104; DB 17; Length 1585;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;

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; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1901
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: X01394
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1901
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Query Match      100.0%; Score 104; DB 13; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 1070 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGCCAGAAATGCTGC 104
DB 1130 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGCCAGAAATGCTGC 1173
```

RESULT 9

US-10-272-411-4

```
; Sequence 4, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0202
; CURRENT APPLICATION NUMBER: US/10/272.411
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ X01394.1
; DATABASE ENTRY DATE: 1995-03-21
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ BC028148.1
; DATABASE ENTRY DATE: 2002-05-01
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ M35592.1
; DATABASE ENTRY DATE: 1993-04-27
; RELEVANT RESIDUES: (1)..(1643)
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NCBI/ XM_165823.1
; DATABASE ENTRY DATE: 2002-08-01
; RELEVANT RESIDUES: (1)..(1643)
US-10-272-411-4
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```
Query Match      100.0%; Score 104; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 1070 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGCCAGAAATGCTGC 104
DB 1130 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGCCAGAAATGCTGC 1173
```

RESULT 10

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US-10-218-547-3
; Sequence 3, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases R
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
US-10-218-547-3
```

```
Query Match      100.0%; Score 104; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 1070 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGCCAGAAATGCTGC 104
DB 1130 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGCCAGAAATGCTGC 1173
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RESULT 11

```
US-10-272-328A-4
; Sequence 4, Application US/10272328A
; Publication No. US20030109444A1
; GENERAL INFORMATION:
; APPLICANT: Barnes Jewish Hospital
; APPLICANT: Lam, Jonathan
; APPLICANT: Ross, F. Patrick
; APPLICANT: Teitelbaum, Steven
; TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
; FILE REFERENCE: 60019620-0206
; CURRENT APPLICATION NUMBER: US/10/272,328A
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 60/329,393
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-328A-4
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Query Match      100.0%; Score 104; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 1070 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGCCAGAAATGCTGC 104
DB 1130 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGCCAGAAATGCTGC 1173
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```
RESULT 12
US-10-310-793-9
; Sequence 9, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating To Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: P573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 9
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: human
US-10-310-793-9

Query Match 100.0%; Score 104; DB 15; Length 1643;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 1070 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129
QY 61 GAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
DB 1130 GAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 1173

RESULT 13
US-10-247-671-68
; Sequence 68, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
```

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; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 68
; LENGTH: 1666
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 223092.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1347, 1358
; OTHER INFORMATION: a, t, c, g, or other
US-10-247-671-68

Query Match 100.0%; Score 104; DB 15; Length 1666;
Best Local Similarity 100.0%; Pred. No. 1.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 1085 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1144
QY 61 GAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
DB 1145 GAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 1188

RESULT 14
US-09-973-850-1
; Sequence 1, Application US/09973850
; Publication No. US20020086016A1
; GENERAL INFORMATION:
; APPLICANT: Wunderink, Richard
; APPLICANT: Waterer, Grant
; TITLE OF INVENTION: Method for Identifying Increased Risk of Death from Community Ac
; TITLE OF INVENTION: Pneumonia
; FILE REFERENCE: GCI-0017
; CURRENT APPLICATION NUMBER: US/09/973,850
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/239,133
; PRIOR FILING DATE: 2000-10-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 2088
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-973-850-1

Query Match 100.0%; Score 104; DB 13; Length 2088;
Best Local Similarity 100.0%; Pred. No. 1.2e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 1506 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1565
QY 61 GAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 104
DB 1566 GAATCTGGAGACAGGAGCCTTTGGTTCTTGGCCAGAAATGCTGC 1609

RESULT 15
US-09-973-850-2
; Sequence 2, Application US/09973850
; Publication No. US20020086016A1
; GENERAL INFORMATION:
; APPLICANT: Wunderink, Richard
; APPLICANT: Waterer, Grant
; TITLE OF INVENTION: Method for Identifying Increased Risk of Death from Community Ac
; TITLE OF INVENTION: Pneumonia
; FILE REFERENCE: GCI-0017
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/ CURRENT APPLICATION NUMBER: US/09/973,850
/ CURRENT FILING DATE: 2001-10-10
/ PRIOR APPLICATION NUMBER: US 60/239,133
/ PRIOR FILING DATE: 2000-10-10
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2
/ LENGTH: 2088
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-09-973-850-2

Query Match      100.0%; Score 104; DB 13; Length 2088;
Best Local Similarity 100.0%; Pred. No. 1.2e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
Db      1506 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1565

QY      61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGCGCAGAAATGCTGC 104
Db      1566 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGCGCAGAAATGCTGC 1609
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Search completed: September 13, 2004, 16:11:24
Job time : 389.578 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 13, 2004, 02:02:56 ; Search time 61.551 Seconds
(without alignments)
937.676 Million cell updates/sec

Title: US-09-801-371A-1

Perfect score: 104

Sequence: 1 gaattcaactggggcctcc.....ggttctggccgaatgctgc 104

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	104	100.0	787	4	US-09-032-297A-13
2	104	100.0	787	4	US-09-229-151C-7
3	104	100.0	1585	4	US-09-023-655-1329
4	104	100.0	1643	3	US-08-880-342-36
5	104	100.0	1643	4	US-09-505-250-4
6	104	100.0	2270	4	US-09-229-151C-13
7	104	100.0	2570	4	US-09-229-151C-14
8	104	100.0	3634	3	US-09-166-186-1
9	104	100.0	3634	3	US-09-313-932-1
10	104	100.0	3634	3	US-09-109-663-34
11	32.6	31.3	2623	4	US-09-976-594-142
12	28	26.9	28720	4	US-09-341-587-7
13	27.4	26.3	116592	4	US-09-818-512-3
14	27.2	26.2	412	4	US-09-621-976-19072
15	26.4	25.4	3170	4	US-09-169-768-1
16	26.4	25.4	3171	4	US-09-169-768-15
17	26.4	25.4	3181	1	US-08-655-086-1
18	26.4	25.4	3349	4	US-09-169-768-13
19	26.4	25.4	3531	4	US-09-169-768-7
20	26.4	25.4	3541	4	US-09-169-768-9
21	26.4	25.4	4409	4	US-09-331-347C-22
22	25.8	24.8	3889	4	US-09-484-970B-39
23	25.8	24.8	4031	1	US-08-159-784-1
24	25.6	24.6	642	3	US-09-328-111-82
25	25.6	24.6	1923	4	US-08-620-312D-1004
26	25.6	24.6	2634	3	US-08-911-853-30
27	25.6	24.6	2634	3	US-09-479-409-30

C 28 25.6 24.6 2634 4 US-09-479-453-30 Sequence 30, Appl
C 29 25.6 24.6 17612 3 US-08-911-853-29 Sequence 29, Appl
C 30 25.6 24.6 17612 3 US-09-479-409-29 Sequence 29, Appl
C 31 25.6 24.6 17612 4 US-09-479-453-29 Sequence 29, Appl
32 25.4 24.4 220 3 US-09-263-933-22 Sequence 22, Appl
33 25.4 24.4 220 4 US-09-919-901-22 Sequence 22, Appl
34 25.4 24.4 604 3 US-09-068-880-14 Sequence 1, Appl
35 25.4 24.4 1026 3 US-09-088-880-14 Sequence 14, Appl
36 25.4 24.4 1289 4 US-09-247-155-138 Sequence 138, App
37 25.4 24.4 1467 3 US-09-330-317B-17 Sequence 17, Appl
38 25.4 24.4 1467 4 US-09-808-589A-17 Sequence 17, Appl
39 25.4 24.4 1956 3 US-08-867-352-20 Sequence 20, Appl
40 25.4 24.4 4145 1 US-08-314-917-1 Sequence 1, Appl
41 25.4 24.4 4145 1 US-08-285-046-1 Sequence 1, Appl
42 25.4 24.4 4145 2 US-08-485-522-1 Sequence 1, Appl
43 25.4 24.4 4145 5 PCT-US93-11401-1 Sequence 1, Appl
44 25.4 24.4 4145 5 PCT-US95-07849-1 Sequence 1, Appl
45 25.4 24.4 4951 2 US-08-752-307B-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-032-297A-13
; Sequence 13, Application US/09032297A
; Patent No. 6525184
; GENERAL INFORMATION:
; APPLICANT: Revati J. Tatake, Steven D. Marlin and
; Randall W. Barton
; TITLE OF INVENTION: Self-Regulated Apoptosis of
; Inflammatory Cells by Gene Therapy

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Boehringer Ingelheim Corporation
STREET: 900 Ridgebury Road, P.O. Box 368
CITY: Ridgefield

STATE: Connecticut
COUNTRY: United States of America
ZIP: 06877-0368

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette

COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS

SOFTWARE: Word Processing
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/032,297A
FILING DATE: 27-Feb-1998

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/038,266
FILING DATE: 28-FEB-97

ATTORNEY/AGENT INFORMATION:
NAME: Robert P. Raymond

REGISTRATION NUMBER: 25089
REFERENCE/DOCKET NUMBER: 9/121PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-791-6183

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

LENGTH: 787
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: <Unknown>
DESCRIPTION: DNA

FEATURE:
NAME/KEY: TNFa 3' untranslated region

SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-032-297A-13

Query Match 100.0%; Score 104; DB 4; Length 787;
Best Local Similarity 100.0%; Fred. No. 2.4e-27;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 222 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 281

QY 61 GAATCTGGAGACACAGGAGCCCTTTGGTTCTGCGCCAGAAATGCTGC 104
DB 282 GAATCTGGAGACACAGGAGCCCTTTGGTTCTGCGCCAGAAATGCTGC 325

RESULT 2

US-09-229-151C-7
; Sequence 7, Application US/09229151C
; Patent No. 6537784
; GENERAL INFORMATION:
; APPLICANT: Tatake, Revati J.
; APPLICANT: Marlin, Steven D.
; APPLICANT: Barton, Randall W.
; TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
; FILE REFERENCE: 9/137
; CURRENT APPLICATION NUMBER: US/09/229,151C
; CURRENT FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: US 60/076,316
; PRIOR FILING DATE: 1998-02-27
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 7
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; OTHER INFORMATION: TNF-alpha untranslated region
US-09-229-151C-7

Query Match 100.0%; Score 104; DB 4; Length 787;

Best Local Similarity 100.0%; Pred. No. 2.4e-27;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 222 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 281

QY 61 GAATCTGGAGACACAGGAGCCCTTTGGTTCTGCGCCAGAAATGCTGC 104
DB 282 GAATCTGGAGACACAGGAGCCCTTTGGTTCTGCGCCAGAAATGCTGC 325

RESULT 3

US-09-023-655-1329
; Sequence 1329, Application US/09023655
; Patent No. 6607873
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1329:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1585 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G339737
; US-09-023-655-1329

Query Match 100.0%; Score 104; DB 4; Length 1585;

Best Local Similarity 100.0%; Pred. No. 3e-27;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1062

QY 61 GAATCTGGAGACACAGGAGCCCTTTGGTTCTGCGCCAGAAATGCTGC 104
DB 1063 GAATCTGGAGACACAGGAGCCCTTTGGTTCTGCGCCAGAAATGCTGC 1106

RESULT 4

US-08-880-342-36
; Sequence 36, Application US/08880342
; Patent No. 8218179
; GENERAL INFORMATION:
; APPLICANT: Webster, Keith A.
; APPLICANT: Bishopric, Nanette H.
; APPLICANT: Murphy, Brian
; APPLICANT: Laderoute, Keith R.
; APPLICANT: Green, Christopher J.
; TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
; TITLE OF INVENTION: Therapeutic Constructs
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/880,342
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB95/00996
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/365,486
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:

/ NAME: Sholtz, Charles K.
/ REGISTRATION NUMBER: 38,615
/ REFERENCE/DOCKET NUMBER: 8255-0018.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1643 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: TNF cDNA HSTNFR (EMBL Accession
/ INDIVIDUAL ISOLATE: #X01394)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 153..851
/ US-08-880-342-36

Query Match 100.0%; Score 104; DB 3; Length 1643;
Best Local Similarity 100.0%; Pred. No. 3.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 60
DB 1070 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1130 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1173

RESULT 5

US-09-505-250-4
/ Sequence 4, Application US/09505250A
/ Patent No. 6329148
/ GENERAL INFORMATION:
/ APPLICANT: Rosen, Glenn
/ APPLICANT: Kao, Peter
/ TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with
/ TITLE OF INVENTION: Triptolides and Death Domain Ligands
/ FILE REFERENCE: SUN-109PRV2
/ CURRENT APPLICATION NUMBER: US/09/505,250A
/ CURRENT FILING DATE: 2000-02-15
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 1643
/ TYPE: DNA
/ ORGANISM: H. sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (153)...(854)
/ US-09-505-250-4

Query Match 100.0%; Score 104; DB 4; Length 1643;
Best Local Similarity 100.0%; Pred. No. 3.1e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 60
DB 1070 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1130 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1173

RESULT 6

US-09-229-151C-13
/ Sequence 13, Application US/09229151C
/ Patent No. 6537784
/ GENERAL INFORMATION:
/ APPLICANT: Tatake, Revati J.
/ APPLICANT: Marlin, Steven D.
/ APPLICANT: Barton, Randall W.
/ TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
/ FILE REFERENCE: 9/137
/ CURRENT APPLICATION NUMBER: US/09/229,151C
/ CURRENT FILING DATE: 1999-01-12
/ PRIOR APPLICATION NUMBER: US 60/076,316
/ PRIOR FILING DATE: 1998-02-27
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patent in version 2.0
/ SEQ ID NO 13
/ LENGTH: 2270
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ OTHER INFORMATION: chimeric gene : -706TNFpGB3'UTR
/ US-09-229-151C-13

Query Match 100.0%; Score 104; DB 4; Length 2270;
Best Local Similarity 100.0%; Pred. No. 3.4e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 60
DB 1705 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 1764

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 1765 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1808

RESULT 7

US-09-229-151C-14
/ Sequence 14, Application US/09229151C
/ Patent No. 6537784
/ GENERAL INFORMATION:
/ APPLICANT: Tatake, Revati J.
/ APPLICANT: Marlin, Steven D.
/ APPLICANT: Barton, Randall W.
/ TITLE OF INVENTION: Self-Regulated Apoptosis of Inflammatory Cells by Gene Therapy
/ FILE REFERENCE: 9/137
/ CURRENT APPLICATION NUMBER: US/09/229,151C
/ CURRENT FILING DATE: 1999-01-12
/ PRIOR APPLICATION NUMBER: US 60/076,316
/ PRIOR FILING DATE: 1998-02-27
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: Patent in version 2.0
/ SEQ ID NO 14
/ LENGTH: 2570
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ OTHER INFORMATION: chimeric gene : -1005TNFpGB3'UTR
/ US-09-229-151C-14

Query Match 100.0%; Score 104; DB 4; Length 2570;
Best Local Similarity 100.0%; Pred. No. 3.6e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 60
DB 2005 GAATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTGTGATCCCTGACATCTG 2064

QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 2065 GAATCTGGAGACCCAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 2108

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RESULT 8
US-09-166-186-1
; Sequence 1, Application US/09166186A
; Patent No. 6080580
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTI-SENSE OLIGONUCLEOTIDE MODULATION OF TNF-a EXPRESSION
; FILE REFERENCE: ISPH-0322
; CURRENT APPLICATION NUMBER: US/09/166,186A
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 250
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1635)..(1821)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1822)..(1869)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1870)..(2070)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes: structure,
; homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
US-09-166-186-1

Query Match 100.0%; Score 184; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 4e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 2808 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 2867

QY 61 GAATTCGAGACAGGAGCCTTTGTTTCTTGCCAGAAATGCTGC 104
DB 2868 GAATTCGAGACAGGAGCCTTTGTTTCTTGCCAGAAATGCTGC 2911

RESULT 9
US-09-313-932-1
; Sequence 1, Application US/09313932A
; Patent No. 6228642
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTI-SENSE OLIGONUCLEOTIDE MODULATION OF TNF-
; FILE REFERENCE: ISPH-0356
; CURRENT APPLICATION NUMBER: US/09/313,932A
; CURRENT FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 501
; SEQ ID NO 1
; LENGTH: 3634
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: CDS
; LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (615)..(981)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (982)..(1588)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1589)..(1634)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1635)..(1821)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (1822)..(1869)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (1870)..(2070)
; FEATURE:
; NAME/KEY: exon
; LOCATION: (2171)..(3381)
; PUBLICATION INFORMATION:
; AUTHORS: Nedwin, G.E.
; AUTHORS: Naylor, S.L.
; AUTHORS: Sakaguchi, A.Y.
; AUTHORS: Smith, D.
; AUTHORS: Jarrett-Nedwin, J.
; AUTHORS: Pennica, D.
; AUTHORS: Goeddel, D.V.
; AUTHORS: Gray, P.W.
; TITLE: Human lymphotoxin and tumor necrosis factor genes:
; structure, homology and chromosomal localization
; JOURNAL: Nucleic Acids Res.
; VOLUME: 13
; ISSUE: 17
; PAGES: 6361-6373
; DATE: 1985-09-11
; DATABASE ACCESSION NUMBER: X02910 Genbank
; DATABASE ENTRY DATE: 1997-02-17
US-09-313-932-1

Query Match 100.0%; Score 104; DB 3; Length 3634;
Best Local Similarity 100.0%; Pred. No. 4e-27;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
DB 2808 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 2867
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QY 4 TTCAAAGCTGGGCGCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTCGAA 63

Dh 81506 TCCAAACTATTGCCACGTAGCTTCCTGTTTCCCATCATATTTTCAACCAGAGAAATATTAT 81565

QY 54 TCTGGAGACCGAGGAGCCTTTGTTCTGGCCAGATCTGTC 104
Db 81566 TTTTCTTTCCAGGGAGGCATTAGCAGTACCCCTGGAAGCTCC 81606

RESULT 14
US-09-621-976-19072/c
; Sequence 19072, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 19072
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 87,95..98,125,239
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-19072

Query Match 26.2%; Score 27.2; DB 4; Length 412;
Best Local Similarity 55.6%; Pred. No. 2.2; Mismatches 1; Indels 0; Gaps 0;
Matches 50; Conservative 1;
QY 3 ATTCAAACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTGGA 62
Db 224 ATAAAGAAGAGGAGCCTCGGCCAGGACGGTGGCTCACACCTGTAAATCCCAACACTTTGGG 165
QY 63 ATCTGAGACCGAGGAGCCTTTGTTCTGG 92
Db 164 AGSCCAGGCGGGCGGACACAGGCTCTGG 135

RESULT 15
US-09-169-768-1
; Sequence 1, Application US/09169768
; Patent No. 6492508
; GENERAL INFORMATION:
; APPLICANT: GRUSKIN, ELLIOT A.
; APPLICANT: BUECHTER, DOUGLAS
; APPLICANT: BROKAW, JANE
; APPLICANT: ZHANG, GUANGHUI
; APPLICANT: PROLELLA, DAVID
; TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DILWORTH & BARRESE
; STREET: 333 EARLE OVINGTON BOULEVARD
; CITY: UNIONDALE
; STATE: NY
; COUNTRY: U.S.A.
; ZIP: 11553
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,768
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEEN, JEFFREY S

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 228-8484
; TELEFAX: (516) 228-8516
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3170 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-169-768-1

Query Match 25.4%; Score 26.4; DB 4; Length 3170;
Best Local Similarity 57.1%; Pred. No. 8.5;
Matches 48; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 8 AACTGGGGCTCCAGAACTCACTGGGGCTTACAGCTTTGATCCCTGACATCTTGGATCTG 67
Db 1307 AGCAGGTGTTCCGGACCCCTGGCGCTGTGCTGCTGGCCAAAGATGAGAGGCTG 1365
QY 68 GAGACCAGGAGCCTTTGTTCTG 91
Db 1367 GAGCTCAGGAGCCCTCGCCCTG 1390

Search completed: September 13, 2004, 13:20:33
Job time : 62.551 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 2, 2004, 02:56:08 ; Search time 372.136 Seconds
(without alignments)
1187.234 Million cell updates/sec

Title: US-09-801-371A-1

Perfect score: 104

Sequence: 1 gaattcaactgggctcc.....ggttctggcagaatgctgc 104

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: N_Geneseq_29Jan04:*
2: Geneseq1980s:*
3: Geneseq1990s:*
4: Geneseq2000s:*
5: Geneseq2001as:*
6: Geneseq2001bs:*
7: Geneseq2002s:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	104	3	Aaz99816 Cis-actin
2	104	100.0	787	2	Aaz20979 Human TNF
3	104	100.0	1275	1	Aan60558 Sequence
4	104	100.0	1323	1	Aan60363 Sequence
5	104	100.0	1324	3	Aaa34963 Human ade
6	104	100.0	1324	3	Aaf21085 Human low
7	104	100.0	1324	7	Abz96779 Human nuc
8	104	100.0	1560	1	Aan80213 Sequence
9	104	100.0	1585	1	Aan60557 Sequence
10	104	100.0	1585	7	Acas4836 Human TNF
11	104	100.0	1606	1	Aan60446 Sequence
12	104	100.0	1606	2	Aat15424 Human tum
13	104	100.0	1643	2	Aat31021 Human tum
14	104	100.0	1643	6	Abk13195 Human tum
15	104	100.0	1643	7	Acc57575 Polynucle
16	104	100.0	1643	7	Aal53712 Tumour ne
17	104	100.0	1643	7	Aad49644 Human tum
18	104	100.0	1643	9	Adc35185 Human CDN
19	104	100.0	1650	7	Acf64375 Human TNF
20	104	100.0	1666	9	Ades5664 Human cDN
21	104	100.0	2270	2	Aaz20983 Chimeric
22	104	100.0	2570	2	Aaz20984 Chimeric
23	104	100.0	3634	2	Aav39005 TNF-alpha

24	104	100.0	3634	2	Aax09014 Tumour ne
25	104	100.0	3634	3	Aaa40760 Human tum
26	104	100.0	3634	3	Aac63770 Human TNF
27	104	100.0	3634	7	Acf63382 Human TNF
28	104	100.0	3634	7	Acc57891 Human tum
29	104	100.0	3634	7	Acas4946 Human TNF
30	104	100.0	3634	6	AcD04988 DNA encod
31	104	100.0	6911	6	Aad45858 Human tum
32	104	100.0	6911	6	Aad45898 Human tum
33	104	100.0	7112	4	Aaf86085 Lymphotox
34	104	100.0	7112	5	Aaf57450 Human tum
35	104	100.0	7112	7	Aal51863 Human tum
36	104	100.0	16310	3	Aaa34964 Human ade
37	104	100.0	16310	3	Aaf21086 Human low
38	104	100.0	16310	7	Abz96780 Human nuc
39	104	100.0	17634	3	Aaa34965 Human ade
40	104	100.0	17634	3	Aaa34965 Human ade
41	104	100.0	17634	3	Aaf21087 Human low
42	104	100.0	17634	3	Aaf21087 Human low
43	104	100.0	17634	7	Abz96781 Human nuc
44	104	100.0	17634	7	Abz96781 Human nuc
45	104	100.0	81800	6	Abk84756 Human CDN

ALIGNMENTS

RESULT 1

Aaz99816
ID AAZ99816 standard; RNA; 104 BP.

XX AC AAZ99816;

XX DT 12-JUL-2000 (first entry)

XX DE Cis-acting nucleotide sequence derived from human TNF-alpha.

XX KW Cis-acting sequence; intron removal; trans-acting factor; alpha-subunit;
RNA-activated protein kinase; eukaryotic initiation factor 2; eif2alpha;
tumour necrosis factor alpha; TNF-alpha; gene therapy; ss.

XX OS Homo sapiens.

XX PN WO200014255-A1.

XX PD 16-MAR-2000.

XX PF 06-SEP-1999; 99WO-IL000483.

XX PR 07-SEP-1998; 98IL-00126112.

XX PR 26-OCT-1998; 98IL-00126757.

XX PA (YISS) YISSUM RES & DEV CO.

XX PI Kaempfer R, Osman F, Jarrous N, Ben-Asouli Y;

XX DR WPI; 2000-257000/22.

XX PT Regulation of gene expression by mRNA splicing is carried out using a cis-acting nucleotide sequence controlled by phosphorylation of the alpha-subunit of eukaryotic initiation factor 2.

XX PS Claim 4; Page 15; 75pp; English.

XX CC The specification describes a cis-acting nucleotide sequence which is capable of removing introns from a precursor transcript encoded by a gene which harbours at least one cis-acting nucleotide sequence. This removal is effected during the production of mRNA of the gene, and depends on activation of a trans-acting factor which is an RNA-activated protein kinase capable of phosphorylating the alpha-subunit of eukaryotic initiation factor 2 (eif2alpha). Insertion of a cis-acting nucleotide sequence, derived from the 3' untranslated region (3'UTR) of the human tumour necrosis factor alpha (TNF-alpha) gene, into another gene renders

CC splicing of precursor transcripts encoded by that gene sensitive to the
 CC level of RNA-activated protein kinase (PKR) activity. The sequence can be
 CC used to transform host cells to regulate gene expression at the mRNA
 CC splicing level, for gene therapy, and to produce a recombinant
 CC therapeutic (e.g. an enzyme, hormone, growth factor, cytokine, structural
 CC protein) or industrially or agriculturally applicable protein. The
 CC present sequence represents a cis-acting nucleotide sequence of the
 CC invention

XX Sequence 104 BP; 23 A; 28 C; 29 G; 24 T; 0 U; 0 Other;
 SQ

Query Match 100.0%; Score 104; DB 3; Length 104;
 Best Local Similarity 100.0%; Pred. No. 2.2e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCARACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60

Db 1 GAATTCARACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60

QY 61 GAATCTGGAGACAGGAGCCCTTGGTTCTGCCAGAAATGCTGC 104

Db 61 GAATCTGGAGACAGGAGCCCTTGGTTCTGCCAGAAATGCTGC 104

RESULT 2

AAZ20979
 ID AAZ20979 standard; DNA; 787 BP.

XX AC AAZ20979;

DT 30-NOV-1999 (first entry)

XX DE Human TNFalpha 3'UTR.

XX KW TNFalpha; tumour necrosis factor alpha; apoptosis; inflammation;
 KW chimeric; multiple sclerosis; Crohn's disease; ulcerative colitis;
 KW psoriasis; graft versus host disease; lupus erythematosus; diabetes;
 KW ankylosing spondylitis; rheumatoid arthritis; ds.

XX OS Homo sapiens.

XX PN WO9943840-A1.

XX PD 02-SEP-1999.

XX PF 12-JAN-1999; 99WO-US000637.

XX PR 27-FEB-1998; 98US-0076316P.

XX PA (BOEH) BOEHRINGER INGELHEIM PHARM INC.

XX PI Tatake RJ, Marlin SD, Barton RW;

XX DR WPI; 1999-527630/44.

XX PT A chimeric polynucleotide consisting of a tissue necrosis factor (TNF)
 XX promoter and an apoptosis-inducing Granzyme B polynucleotide.

XX PS Example 1; Page 60-61; 71pp; English.

XX CC This sequence represents a human TNFalpha (tumour necrosis factor alpha)
 CC 3'UTR (untranslated region). Chimeric nucleotides (AAZ20983, 220984) were
 CC constructed comprising at least one TNFalpha promoter enhancer region
 CC (AAZ20975-220978), a TNFalpha promoter (AAZ20972-220974), a DNA encoding
 CC the apoptosis-inducing Granzyme B protein (AAZ20982), and a TNFalpha
 CC 3'UTR sequence. TNFalpha is one of a number of cytokines produced by
 CC inflammatory cells. Upregulation and/or dysregulation of cytokines in
 CC inflamed tissue may be directly or indirectly responsible for
 CC exacerbation of chronic inflammatory diseases. Introduction of the
 CC chimeric nucleotide to activated inflammatory cells causes them to
 CC undergo apoptosis. Pharmaceutical compositions of the chimeric nucleotide
 CC may be useful for treating inflammatory disorders such as multiple
 CC sclerosis, Crohn's disease, ulcerative colitis, psoriasis, graft versus

CC host disease, lupus erythematosus, insulin-dependent (type I) diabetes
 CC mellitus, ankylosing spondylitis, and in particular, rheumatoid
 CC arthritis. The use of such chimeric nucleotides offers simpler and
 CC cheaper long-term relief, in comparison with existing conventional
 CC pharmaceutical and invasive surgery methods

XX Sequence 787 BP; 190 A; 204 C; 172 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 2; Length 787;

Best Local Similarity 100.0%; Pred. No. 3.9e-25;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCARACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60

Db 222 GAATTCARACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 281

QY 61 GAATCTGGAGACAGGAGCCCTTGGTTCTGCCAGAAATGCTGC 104

Db 282 GAATCTGGAGACAGGAGCCCTTGGTTCTGCCAGAAATGCTGC 325

RESULT 3

AAZ60558
 ID AAZ60558 standard; DNA; 1275 BP.

XX AC AAZ60558;

DT 28-JUL-1991 (first entry)

XX DE Sequence encoding mature human tumour necrosis factor (hTNF) mutein Ser
 XX 69 in pAW731.

XX KW Antitumour; anticancer; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 1..474
 XX /*tag= a

XX PN WC8604606-A.

XX PD 14-AUG-1986.

XX PF 03-FEB-1986; 86WO-US000236.

XX PR 07-FEB-1985; 85US-00698939.

XX PA (CETU) CETUS CORP.

XX PI Mark DF, Lin LS, Lu SDY, Wang AM;

XX DR WPI; 1986-225458/34.

XX DR P-PSDB; AAP60656.

XX PT New synthetic muteins of human tumour necrosis factor protein - are obtd.
 XX by direct mutagenesis and retain antitumour activity.

XX PS Disclosure; Fig 3a; 47pp; English.

XX CC The sequence encoding TNF produced by the promyelocytic leukemia cell
 CC line (HL-60, ATCC no. CCL240) has been cloned and expressed in E.coli (see
 CC AAN60557). Neither of the cysteine residues (69 and 101) in the TNF
 CC sequence appears to be involved in disulphide linkages. The patentors
 CC claim a novel synthetic mutein of a biologically active hTNF protein,
 CC having at least one cysteine residue free from a disulphide link and non-
 CC essential to the activity and having at least one of the cysteines
 CC residues deleted or replaced by another AA. Plasmid pAW731 (Ser 69) is
 CC claimed

XX Sequence 1275 BP; 298 A; 357 C; 308 G; 312 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 1; Length 1275;

Best Local Similarity 100.0%; Pred. No. 4.4e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 60
DB 693 GAATTCAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 752

QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 753 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 796

RESULT 4
ID AAN60363 standard; DNA; 1323 BP.
AC AAN60363;
DT 19-JUN-1991 (first entry)
DE Sequence encoding human tumour necrosis factor.
KW hTNF; tumour; cancer; interferon; ds.

OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..534
FT /tag= a
FT sig_peptide 1..60
FT /tag= b
FT /label= Secretory leader peptide
FT mat_peptide 61..534
FT /tag= c

PN EP168214-A.
XX 15-JAN-1986.
XX 03-JUL-1985; 85EP-00304758.
XX 05-JUL-1984; 84US-00627959.
XX 05-JUL-1984; 84US-00628059.
XX 05-JUL-1984; 84US-00628060.
XX 03-DEC-1984; 84US-00677156.
XX 03-DEC-1984; 84US-00677257.
XX 03-DEC-1984; 84US-00677267.
XX 03-DEC-1984; 84US-00677454.
XX (GETH) GENENTECH INC.

PI Aggarwal BS, Lee SH, Goeddel DV, Nedwin GE;
XX WPI; 1986-015483/03.
XX P-PSDB; AAP60417.
XX Pure tumour necrosis factor and mutant forms - new DNA coding sequences
XX and transformed cells.
XX Claim 20; Fig 10; 90pp; English.
XX Sequence encodes the pure human tumour necrosis factor, mutants of which
XX are covered by the claims. TNF and mutants are useful in treating
XX tumours, especially in tandem with interferon. The encoding sequence may
XX be used to create plasmid pTTPXPTNF, allowing transformation of an
XX E.coli host for the expression of TNF

SQ Sequence 1323 BP; 298 A; 385 C; 310 G; 330 T; 0 U; 0 Other;
Query Match 100.0%; Score 104; DB 1; Length 1323;
Best Local Similarity 100.0%; Pred. No. 4.5e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 60
DB 750 GAATTCAACTGGGCGCTCCAGAACTCACTGGGCGCTACAGCTTTGATCCCTGACATCTG 809

QY 61 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104
DB 810 GAATCTGGAGACCAAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 853

RESULT 5
ID AAA34963 standard; DNA; 1324 BP.
XX AAA34963;
AC AAA34963;
DT 28-JUL-2000 (first entry)
DE Human adenosine receptor related polynucleotide SEQ ID NO:2652.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX phosphorothioate; impaired respiration; inflammation; allergy;
XX allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
XX lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

OS Homo sapiens.
XX WO200009525-A2.
XX 24-FEB-2000.
XX 03-AUG-1999; 99WO-US017712.
XX 03-AUG-1998; 98US-0095212P.
XX (UYEC-) UNIV EAST CAROLINA.
XX Nyce JW;
XX WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
XX vasoconstriction, inflammation, allergies, asthma, hypertension,
XX bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX cancers.

XX Disclosure; Page 814-815; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
XX oligonucleotide (ON) with low adenosine (up to 15%), which targets
XX nucleic acids involved in bronchoconstriction, allergies, and/or
XX inflammation. The ON can have antiinflammatory, antiallergic,
XX antiasthmatic, cyostatic and analgesic activities. The compositions are
XX useful for the treatment of diseases associated with inflammation,
XX impaired airways, including lung disease and diseases whose secondary
XX effects afflict the lungs of a subject. They can be used for treating
XX e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
XX impeded respiration, respiratory distress syndrome, pain, cystic
XX fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX pulmonary disease (COPD) and cancers such as leukaemias, lymphomas,
XX carcinomas, and cancers which may metastasise to the lungs, including
XX breast and prostate cancer. The reduction of the adenosine content of the
XX ON reduces side effects. The A-containing ONs break down with the
XX release of deoxyadenosine which activates adenosine receptors causing the
XX bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
XX nucleotide sequences given in the sequence listing from the present
XX invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
XX sequences are also called SEQ ID NO:1 to 185, but the sequences differ
XX from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
XX AAA33992) are specifically claimed ONs from the present invention. N.B.

CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
 Query Match 100.0%; Score 104; DB 3; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 4.5e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
 Db 751 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810
 QY 61 GAATCTGAGACCCAGGAGCCTTTGGTTCTGGCCAGATGCTGC 104
 Db 811 GAATCTGAGACCCAGGAGCCTTTGGTTCTGGCCAGATGCTGC 854
 RESULT 6
 ID AAF21085 standard; DNA; 1324 BP.
 XX
 AC AAF21085;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human low adenosine antisense oligonucleotide related sequence #2652.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-679539/66.
 XX
 PT Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 PS Disclosure; Page 887; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (i) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (i) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (i) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and

CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX

SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;
 Query Match 100.0%; Score 104; DB 3; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 4.5e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 60
 Db 751 GAATTCAAACTGGGGCCTCCAGAACTCACTGGGGCCTACAGCTTTGATCCCTGACATCTG 810
 QY 61 GAATCTGAGACCCAGGAGCCTTTGGTTCTGGCCAGATGCTGC 104
 Db 811 GAATCTGAGACCCAGGAGCCTTTGGTTCTGGCCAGATGCTGC 854

RESULT 7
 ABZ96779
 ID ABZ96779 standard; DNA; 1324 BP.
 XX
 AC ABZ96779;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human nucleic acid sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiqunone; antiinflammatory; anti-allergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIC-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Disclosure; SEQ ID NO 12021; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 1324 BP; 298 A; 387 C; 308 G; 331 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 7; Length 1324;

Best Local Similarity 100.0%; Pred. No. 4.5e-25;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60

Db 751 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 810

OY 61 GAATCTGGAGACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104

Db 811 GAATCTGGAGACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 854

RESULT 8

AAAN80219

ID AAAN80219 standard; DNA; 1560 BP.

AC AAAN80219;

XX DT 28-DEC-1990 (first entry)

XX Sequence of pE4 encoding human tumour necrosis factor (TNF).

XX Lymphokine; antitumour; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 86..313

FT /*tag= a

FT mat_peptide 314..787

FT /*tag= b

XX WO8806625-A.

XX PD 07-SEP-1988.

XX 25-JAN-1988; 88WO-US000183.

XX 26-FEB-1987; 87US-00019221.

XX (CETU) CETUS CORP.

XX Mark DF, Lin LS, Thomson JW, Yamamoto R;

XX WPI; 1988-271165/38.

XX P-PSDB; AAP80728.

XX

XX Human tumour necrosis factor muteins - having comparable biological

PT activity with improved stability and ease of purification.

XX Disclosure; Fig 1-1 to 1-2; 51pp; English.

XX A human TNF protein which is modified from the sequence shown in

CC AAP80728, including naturally occurring allelic variants is claimed. Also

CC claimed are: recombinant DNA sequences encoding the protein (AAAN80219);

CC and control sequences for expression; a vector; a transformed host cell;

CC a method of producing the protein by culturing the host cell;

CC pharmaceutical compen. of the protein and a carrier and a method of

CC treating tumour burden with the compen. The muteins are capable of the

CC range of biological activities exhibited by native TNF but exhibit

CC improved stability and ease of purification

XX SQ Sequence 1560 BP; 340 A; 473 C; 381 G; 366 T; 0 U; 0 Other;

Query Match 100.0%; Score 104; DB 1; Length 1560;

Best Local Similarity 100.0%; Pred. No. 4.7e-25;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60

Db 1003 GAATTCAACTGGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1062

OY 61 GAATCTGGAGACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 104

Db 1063 GAATCTGGAGACAGGAGCCTTTGGTTCTGGCCAGAAATGCTGC 1106

RESULT 9

AAAN60557

ID AAAN60557 standard; DNA; 1585 BP.

XX AAAN60557;

XX DT 28-JUL-1991 (first entry)

XX Sequence encoding mature human tumour necrosis factor (hTNF) in pE4.

XX Antitumour; anticancer; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 86..313

FT /*tag= a

FT mat_peptide 314..787

FT /*tag= b

XX WO8604606-A.

XX PD 14-AUG-1986.

XX 03-FEB-1986; 86WO-US000236.

XX 07-FEB-1985; 85US-00698939.

XX (CETU) CETUS CORP.

XX Mark DF, Lin LS, Lu SDY, Wang AM;

XX WPI; 1986-225458/34.

XX P-PSDB; AAP60655.

XX

XX New synthetic muteins of human tumour necrosis factor protein - are obtd.

PT by direct mutagenesis and retain antitumour activity.

XX Disclosure; Fig 1; 47pp; English.

XX The sequence encoding TNF produced by the promyelocytic leukemia cell

CC line (HL-60, ATCC no.CCL240) has been cloned and expressed in E.coli (see

CC AAN60557). Neither of the cysteine residues (69 and 101) in the TNF
CC sequence appears to be involved in disulphide linkages. The patentors
CC claim a novel synthetic mutin of a biologically active hTNF protein,
CC having at least one cysteine residue free from a disulphide link and non-
CC essential to the activity and having at least one of the cysteine
CC residues deleted or replaced by another AA. Plasmid pAW731 (Ser 69) is
CC claimed
XX
SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;
Query Match 100.0%; Score 104; DB 1; Length 1585;
Best Local Similarity 100.0%; Pred. No. 4.7e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 60
DB 1003 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 1062
QY 61 GAATCTGAGACCCAGGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
DB 1063 GAATCTGAGACCCAGGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 1106
RESULT 10
ACA64836
ID ACA64836 standard; DNA; 1585 BP.
XX AC ACA64836;
XX 27-JUN-2003 (first entry)
XX Human TNF-alpha DNA corresponding to M10988.
DE Human; chronic inflammatory joint disease; infection; tumour;
XX antiinflammatory; cytostatic; antiarthritic; antirheumatic;
KW immunosuppressive; gene therapy; etiological pathogenicity; ds.
OS Homo sapiens.
XX
XX DE10127572-A1.
XX 05-DEC-2002.
XX 30-MAY-2001; 2001DE-01027572.
XX 30-MAY-2001; 2001DE-01027572.
XX (PATH-) PATHOARRAY GNBH.
XX Haeupl T, Ungethuen U, Blaess S;
XX WPI; 2003-240797/24.
XX Reagents for diagnosis, study and therapy of chronic inflammatory joint
XX and other diseases, comprises any of many specified genes or derived
XX proteins.
XX Claim 1; Page; 12pp; German.
XX This invention describes a novel reagent for diagnosis, molecular
XX definition and therapy of chronic inflammatory joint diseases, and other
XX inflammatory disorders, infective or tumour diseases in humans. The
XX products of the invention have antiinflammatory, cytostatic,
XX antiarthritic, antirheumatic and immunosuppressive activity and can be
XX used for gene therapy. The reagent of the invention and any proteins and
XX antibodies derived from it, are used (i) for analysing tissue and blood
XX samples for medical diagnosis; (ii) for diagnosis and characterisation of
XX chronic joint diseases, on the basis of molecular characterisation, and
XX determining the etiological pathogenicity principle of as yet
XX uncharacterised inflammatory diseases, also monitoring progression and/or
XX treatment of disease, and optimisation of therapy and (iii) for
XX developing treatments for inflammatory diseases, particularly of joints,
XX infections and tumours. ACA64801-ACA64965 represent human polynucleotides

CC used in the method of the invention
XX
SQ Sequence 1585 BP; 352 A; 473 C; 389 G; 371 T; 0 U; 0 Other;
Query Match 100.0%; Score 104; DB 7; Length 1585;
Best Local Similarity 100.0%; Pred. No. 4.7e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 60
DB 1003 GAATTCAAACTGGGGCCCTCCAGAACTCACTGGGGCCCTACAGCTTTGATCCCTGACATCTG 1062
QY 61 GAATCTGAGACCCAGGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 104
DB 1063 GAATCTGAGACCCAGGGAGCCTTTGGTTCTGCGCCAGAAATGCTGC 1106
RESULT 11
AAN60446
ID AAN60446 standard; cDNA; 1606 BP.
XX AC AAN60446;
XX 25-MAR-2003 (revised)
DT 07-AUG-1991 (first entry)
XX
XX Sequence encoding tumour necrosis factor (TNF).
XX Anticancer agent; antitumour; antimalarial; tumour necrosis factor; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 158..859
FT /*tag= a
XX WO8603751-A.
XX 03-JUL-1986.
XX 19-DEC-1985; 85WO-EP000721.
XX 21-DEC-1984; 84US-00684595.
XX 09-OCT-1985; 85US-00785847.
XX 09-OCT-1986; 86WO-US002133.
XX (BIOJ) BIOGEN NV.
XX (FIER/) FIERs W C.
XX (ALLE/) ALLET B.
XX (BIOJ) BIOGEN INC.
XX Fiers WC, Franses LM, Tavernier JHL, Marmenout ALM, Vanderheyd J;
XX Allet B;
XX WPI; 1986-182891/28.
XX P-PSDB; AAP60531.
XX Mammalian tumour necrosis factors - produced by culturing pro-karyotic
XX PT hosts transformed with recombinant DNA.
XX
XX Example; Fig 9; 93pp; English.
XX
XX TNF-like polypeptides and compens. are produced by the fermentation of a
XX host cells transformed with at least one DNA sequence which codes for a
XX mammalian TNF-like polypeptide operatively linked to an expression
XX control sequence in the transformed host. (Updated on 25-MAR-2003 to
XX correct PA field.)
XX
XX Sequence 1606 BP; 357 A; 494 C; 394 G; 361 T; 0 U; 0 Other;
Query Match 100.0%; Score 104; DB 1; Length 1606;
Best Local Similarity 100.0%; Pred. No. 4.7e-25;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAGAGTGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
 |||||
 Db 1075 GAATTCAGAGTGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1134

QY 61 GAATCTGGAGACAGGAGCCTTGGTTCTGCGCAGAAATGCTGC 104
 |||||
 Db 1135 GAATCTGGAGACAGGAGCCTTGGTTCTGCGCAGAAATGCTGC 1178

RESULT 12
 AAT15424
 ID AAT15424 standard; cDNA; 1606 BP.
 XX
 AC AAT15424;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-APR-1996 (first entry)
 XX
 XX Human tumour necrosis factor cDNA clone p-hTNF-1.
 XX
 XX Tumour necrosis factor; TNF; phage T4; phage lambda; pL promoter;
 KW antitumour; anticancer; antimalarial; ss.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 158..859
 FT /*tag= a
 FT sig_peptide 158..385
 FT /*tag= b
 FT mat_peptide 386..856
 FT /*tag= c
 XX
 XX US5487984-A.
 PN
 XX
 XX 30-JAN-1996.
 PD
 XX
 XX 20-DEC-1985; 85US-00811654.
 PF
 XX
 XX 21-DEC-1984; 84US-00684595.
 PR
 XX 09-OCT-1985; 85US-00785847.
 XX
 XX (BIOU) BIOGEN INC.
 PA
 XX
 XX Allet B, Kawashima EH;
 PI
 XX
 XX WPI; 1996-105230/11.
 DR
 XX P-PSDB; AAR88590.
 XX

XX Prodn. of tumour necrosis factor - using recombinant DNA encoding TNF
 PT under the control of T4 or lambda pL-T4 expression control sequences.
 PT
 XX
 XX Example 9; Fig 9; 43pp; English.
 PS
 XX
 XX A cDNA clone (AAT15424), p-hTNF-1 (DSM 3160), codes for the human tumour
 CC necrosis factor (hTNF) precursor (AAR88590). It was obt'd. by screening a
 CC human cDNA library with a fragment of mouse TNF cDNA. The isolated cDNA
 CC may be linked to expression control sequences from phage T4 or phage
 CC lambda (see AAT15402-05 and AAT15425-26) for expression in host cells,
 CC esp. Escherichia coli, and commercial-scale prodn. of recombinant TNF of
 CC use as an antitumour, anticancer and antimalarial agent. (Updated on 25-
 CC MAR-2003 to correct PF field.)
 XX

SQ Sequence 1606 BP; 357 A; 494 C; 394 G; 361 T; 0 U; 0 Other;
 Query Match 100.0%; Score 104; DB 2; Length 1606;
 Best Local Similarity 100.0%; Pred. No. 4.7e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAGAGTGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
 |||||
 Db 1075 GAATTCAGAGTGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1134

QY 61 GAATCTGGAGACAGGAGCCTTGGTTCTGCGCAGAAATGCTGC 104
 |||||
 Db 1135 GAATCTGGAGACAGGAGCCTTGGTTCTGCGCAGAAATGCTGC 1178

RESULT 13
 AAT31021
 ID AAT31021 standard; DNA; 1643 BP.
 XX
 AC AAT31021;
 XX
 DT 26-SEP-1996 (first entry)
 DT
 XX
 XX Human tumour necrosis factor cDNA clone HSTNFR.
 DE
 XX Gene therapy; hypoxia related enhancer element; HREP; ischaemia;
 KW reperfusion; promoter; tumour necrosis factor; TNF; ds.
 XX
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 153..854
 FT /*tag= a
 FT
 XX
 XX WO9620276-A1.
 FN
 XX
 XX 04-JUL-1996.
 PD
 XX
 XX 13-NOV-1995; 95WO-IB000996.
 PF
 XX
 XX 23-DEC-1994; 94US-00365486.
 PR
 XX
 XX (STRI) SRI INT.
 PA
 XX
 XX Webster KA, Bishopric NH, Murphy B, Laderoute KR, Green CJ;
 PI
 XX
 XX WPI; 1996-321849/32.
 DR
 XX P-ESDB; AAW00454.
 XX

XX Chimeric gene contg. therapeutic gene linked to HREE - partic. for
 PT expressing SOD etc in hypoxic tissue to reduce tissue injury caused by
 PT ischaemia or reperfusion.
 PT
 XX
 XX Example 8; Page 100-101; 118pp; English.
 PS
 XX

XX A PCR-generated DNA fragment (AAT31021) encoding human tumour necrosis
 CC factor (hTNF) (AAW00454). hTNF induces apoptosis and is not known to be
 CC induced by hypoxic stress. A -90 bp human metallothionein IIA promoter
 CC fragment (see also AAT31003) was inserted upstream of the hTNF gene and
 CC the construct was used to transfect mouse C2C12 myoblasts and A431 cells.
 CC Hypoxia-mediated TNF induction and tumour control were demonstrated in
 CC an animal xenograft model
 XX
 XX Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 U; 0 Other;

SQ
 Query Match 100.0%; Score 104; DB 2; Length 1643;
 Best Local Similarity 100.0%; Pred. No. 4.7e-25;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCAGAGTGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
 |||||
 Db 1070 GAATTCAGAGTGGGCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129

QY 61 GAATCTGGAGACAGGAGCCTTGGTTCTGCGCAGAAATGCTGC 104
 |||||
 Db 1130 GAATCTGGAGACAGGAGCCTTGGTTCTGCGCAGAAATGCTGC 1173

RESULT 14
 ABK13195
 ID ABK13195 standard; DNA; 1643 BP.
 XX

AC ABX13195;
XX
XX
XX 23-APR-2002 (first entry)
XX
XX Human tumour necrosis factor alpha (TNF alpha) DNA.
XX
XX TNF; apoptosis; ds; tumour; death domain receptor ligand;
XX diterpenoid triepoxide; cytotatic activity; c-IAP2; c-IAP1; carcinoma;
XX mammary adenocarcinoma; non-small cell lung carcinoma;
XX neurological malignancy; haematological malignancy; lichen planus;
XX non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;
XX malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
XX non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
XX T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
XX discoid lupus erythematosus; human; gene; tumour necrosis factor.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 153. .854
FT CDS /*tag= a
FT /*product= "TNF alpha protein"
XX
XX US6329148-B1.
XX
XX 11-DEC-2001.
XX
XX 15-FEB-2000; 2000US-00505250.
XX
XX 16-FEB-1999; 99US-0120313P.
XX 20-AUG-1999; 99US-0149989P.
XX
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX
XX Rosen GD, Kao P;
XX
XX WPI; 2002-121125/16.
XX P-PSDB; AAU75065.
XX
XX Use of a synergistic combination of death domain receptor ligands and
XX diterpenoid triepoxides for killing of tumor cells.
XX
XX Disclosure; Col 27-30; 20pp; English.
XX
XX This invention relates to a novel method for enhanced killing of tumour
XX cells comprising contacting a tumour cell with a synergistic combination
XX of a death domain receptor ligand and a diterpenoid triepoxide. This
XX method has cytostatic activity and works by blocking TNF-alpha mediated
XX induction of c-IAP2 and c-IAP1. The method of the invention may be used
XX for treating tumours, particularly solid tumours, e.g. carcinoma, mammary
XX adenocarcinoma and non-small cell lung carcinoma also neurological
XX malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma,
XX chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis
XX fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-
XX cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid
XX lupus erythematosus, lichen planus. The combination may be administered
XX with other active agents, e.g. anti-metastatic, anti-tumour or anti-
XX angiogenic agents. The potent synergy between the diterpenoids and the
XX death domain ligands allows increased killing at equivalent or lower
XX doses, and can sensitize otherwise resistant cells. This sequence
XX represents the human tumour necrosis factor alpha (TNF alpha) DNA. TNF
XX alpha is a ligand for death domain receptors used in the used method of
XX the invention in combination with diterpenoid triepoxides to kill tumours
XX by induction of apoptosis
XX
XX Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 104; DB 6; Length 1643;
XX Best Local Similarity 100.0%; Pred. No. 4.7e-25;
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GAATTCAACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
XX

Db 1070 GAATTCARACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129
QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTCTGGCCAGAAATGCTGC 104
XX
Db 1130 GAATCTGGAGACCCAGGAGCCTTTGGTTCTCTGGCCAGAAATGCTGC 1173
XX
RESULT 15
ACCS7575
ID ACCS7575 standard; DNA; 1643 BP.
XX
AC ACCS7575;
XX
XX 28-JUL-2003 (first entry)
XX
XX Polynucleotide encoding tumour necrosis factor superfamily member.
XX
XX Human; RANKL; tumour necrosis factor; osteopathic; bone; gene; ds.
XX
XX Homo sapiens.
XX
XX WO2003033663-A2.
XX
XX 24-APR-2003.
XX
XX 15-OCT-2002; 2002WO-US033022.
XX
XX 15-OCT-2001; 2001US-0329393P.
XX
XX (BARN-) BARNES-JEWISH HOSPITAL.
XX
XX Lam J, Ross PF, Teitelbaum SL;
XX
XX WPI; 2003-430346/40.
XX
XX New RANKL mimic comprising a core, and at least one external loop, useful
XX for enhancing processes of bone formation or inhibiting bone resorption,
XX PT thus providing treatments for disease or condition characterized by loss
XX of bone mass.
XX
XX Disclosure; Page 48-49; 78pp; English.
XX
XX The present sequence is that of a polynucleotide encoding a non-RANKL
XX member of the tumour necrosis factor (TNF) superfamily. The invention
XX provides non-naturally-occurring proteins that contain one or more of the
XX external surface loops of RANKL (see ABR42066-70) in combination with a
XX heterologous protein core obtained from a non-RANKL member of the TNF
XX superfamily. Also provided are polynucleotides encoding such proteins.
XX The proteins bind to RANK, acting as mimics of RANKL. They can be used to
XX enhance bone formation by either inhibiting bone resorption or inducing
XX osteogenesis, thus providing treatment for diseases or conditions
XX characterised by loss of bone mass
XX
XX Sequence 1643 BP; 370 A; 495 C; 398 G; 380 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 104; DB 7; Length 1643;
XX Best Local Similarity 100.0%; Pred. No. 4.7e-25;
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GAATTCARACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 60
XX
Db 1070 GAATTCARACTGGGGCCTCCAGAACTCACTGGGGCTACAGCTTTGATCCCTGACATCTG 1129
XX
QY 61 GAATCTGGAGACCCAGGAGCCTTTGGTTCTCTGGCCAGAAATGCTGC 104
XX
Db 1130 GAATCTGGAGACCCAGGAGCCTTTGGTTCTCTGGCCAGAAATGCTGC 1173
XX

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